

NH₃

- COOH

PEPTIDE-ASG₄SG₃ - MHC β CHAIN REGIONS
Linker

FIG. 1A

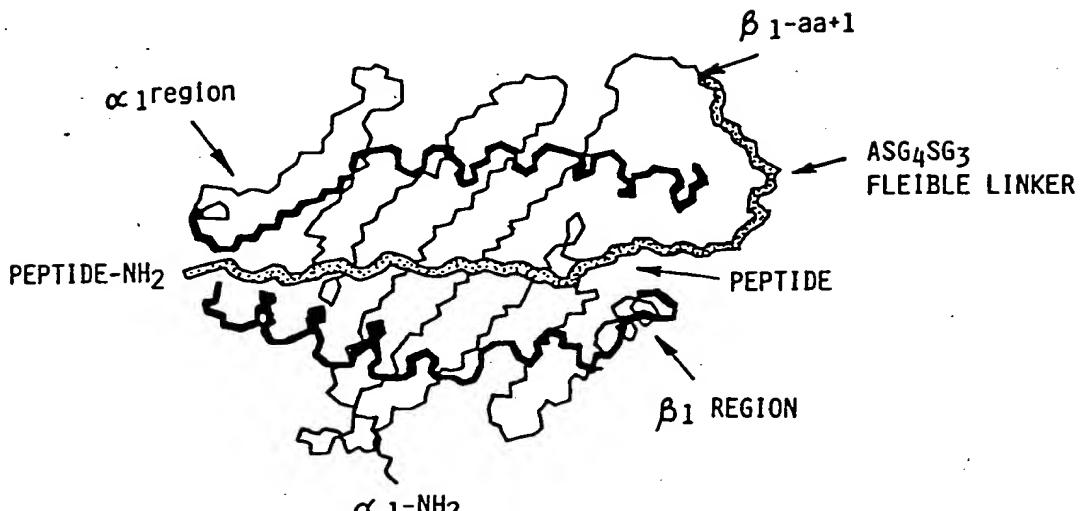


FIG. 1B

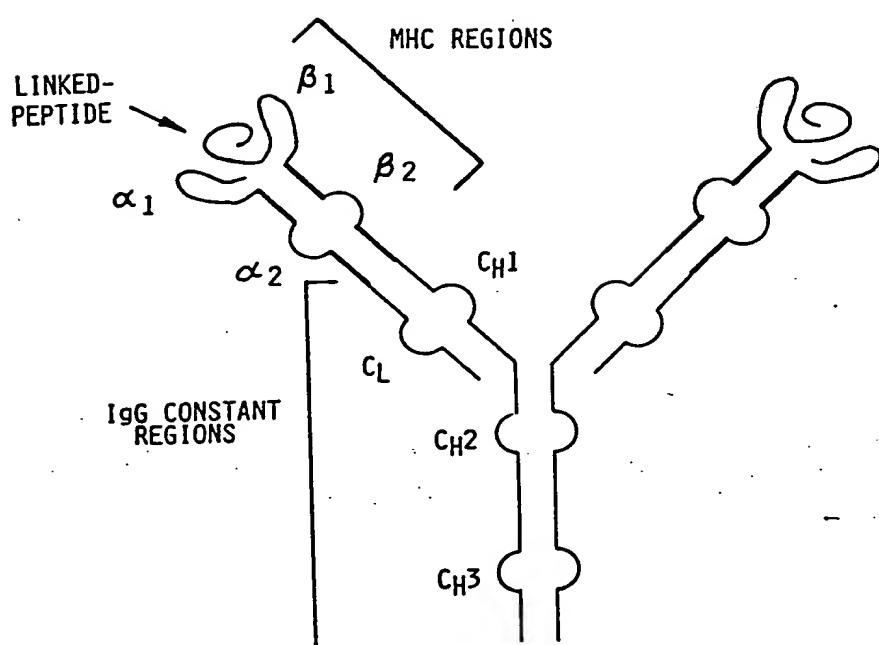
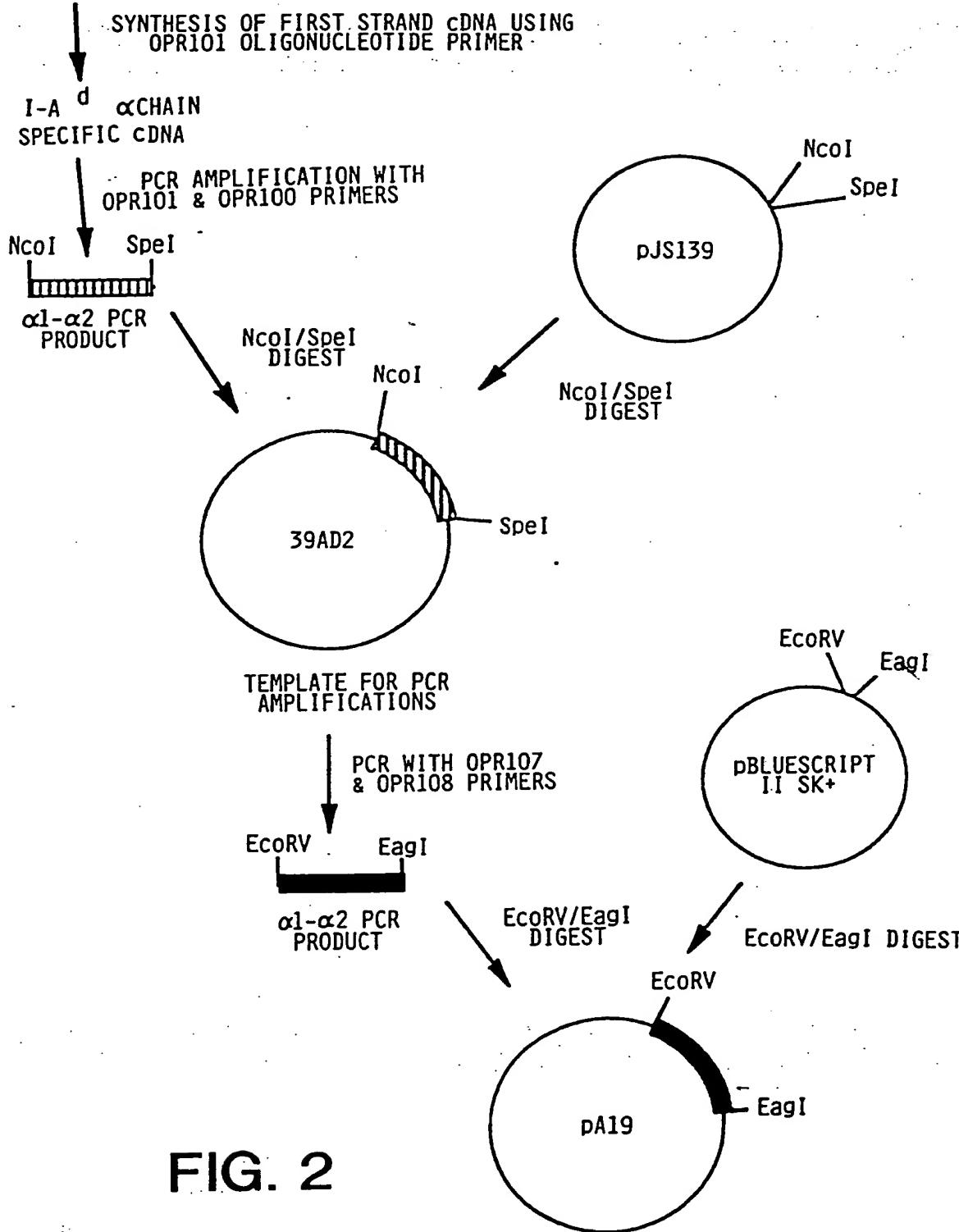


FIG. 1C

09243154-050304

TOTAL RNA ISOLATED
FROM A20 CELLS



RECORDED: 4/16/1990

TOTAL RNA ISOLATED
FROM A20 CELLS

SYNTHESIS OF FIRST STRAND cDNA USING
OLIGO dT PRIMER

cDNA TEMPLATE

PCR AMPLIFICATION WITH
OPR102 & OPR104 PRIMERS

NcoI SpeI
β1-β2 PCR
PRODUCT

NcoI/SpeI
DIGEST

NcoI
pJS139
SpeI

NcoI
39BD2
SpeI

TEMPLATE FOR PCR
AMPLIFICATIONS

PCR WITH OPR106
& OPR112 PRIMERS

EcoRV EagI
NheI
AflII
Linker-β1-β2
PCR PRODUCT

EcoRV/EagI
DIGEST

EcoRV
EagI
pBLUESCRIPT
II SK+

EcoRV EagI
DIGEST

HINDIII
AflII
NheI
EagI
pB15

MUTATION IN LINKER REGION-
NO ECO RV SITE PRESENT

FIG. 3A

09848674 09848675 09848676

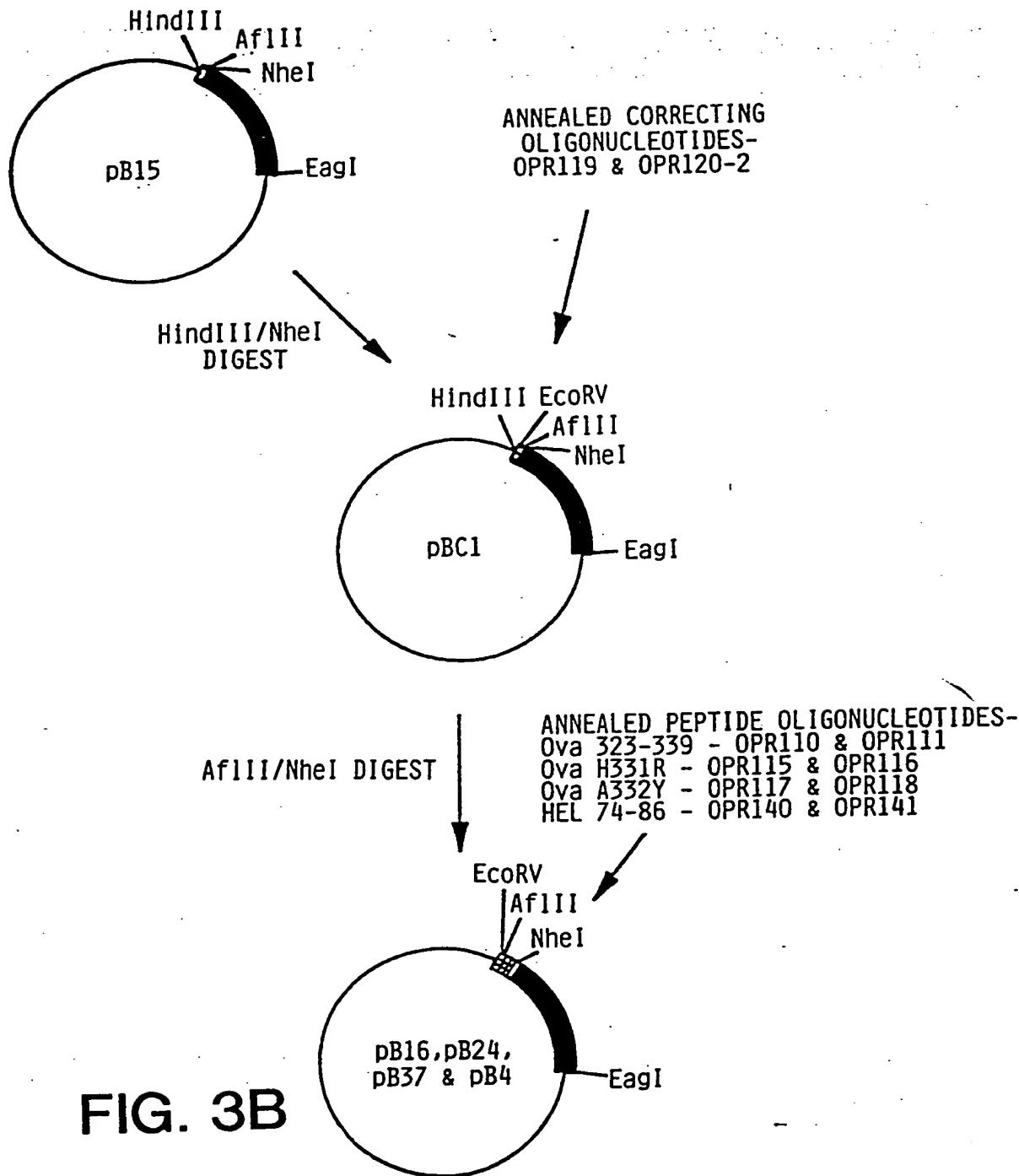


FIG. 3B

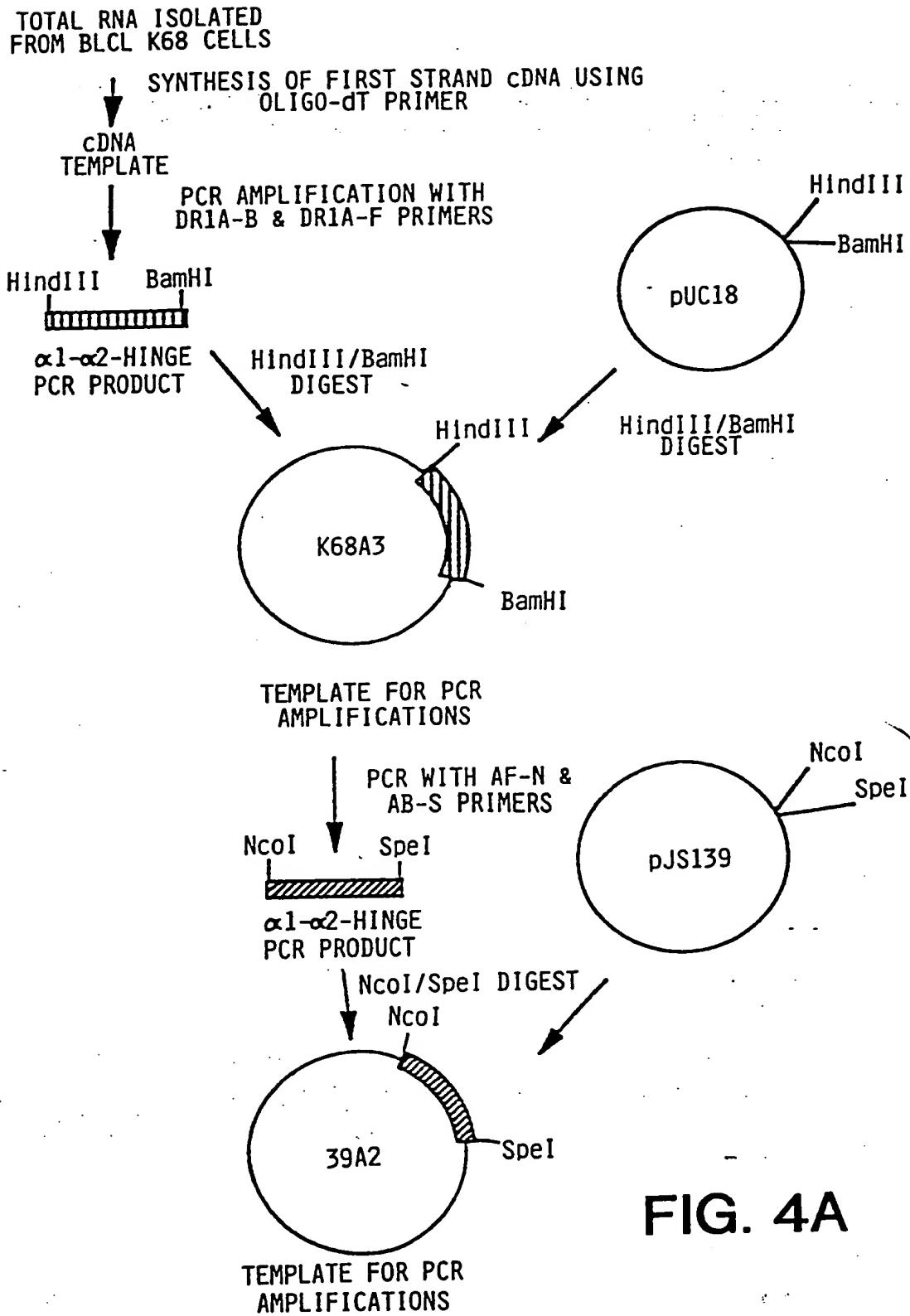


FIG. 4A

REPRODUCED BY OPTICAL SCANNER

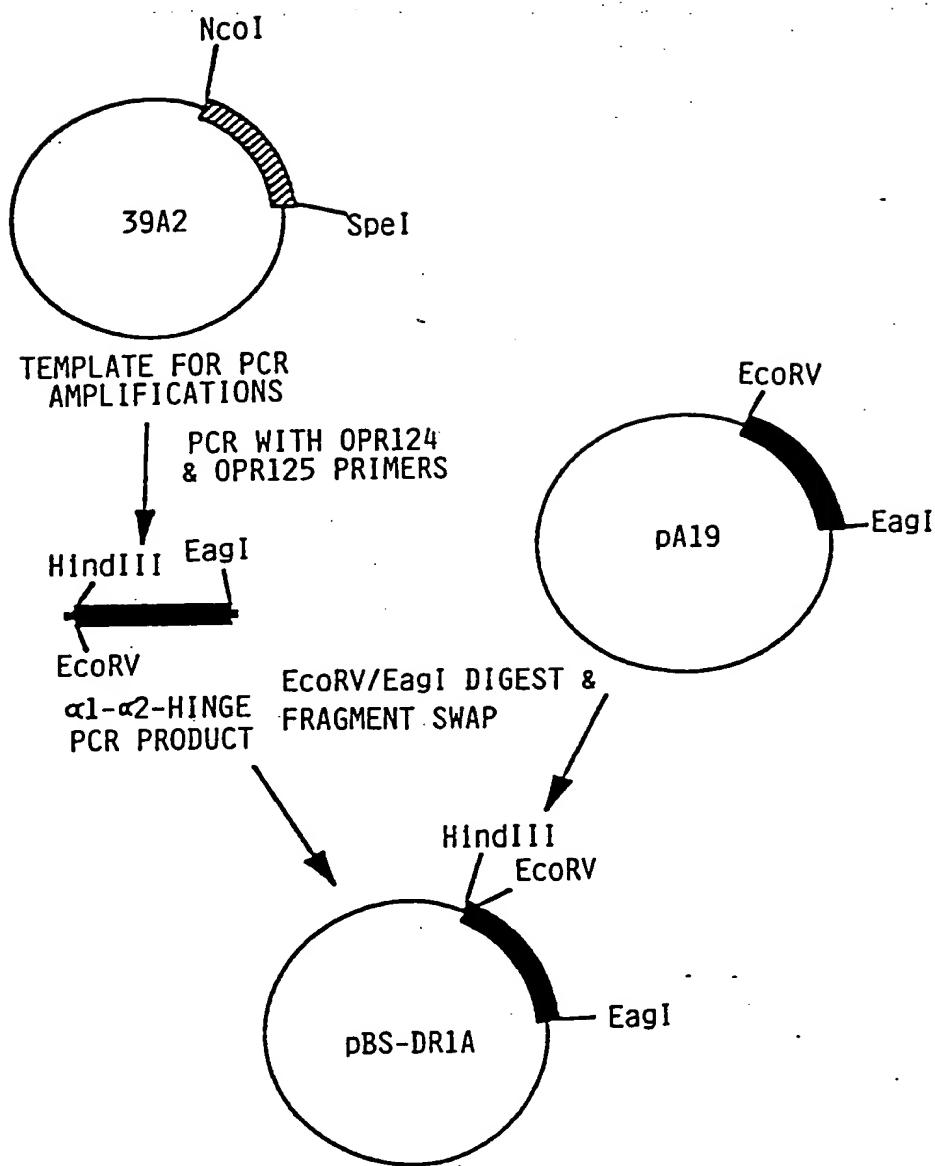
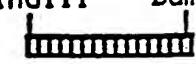
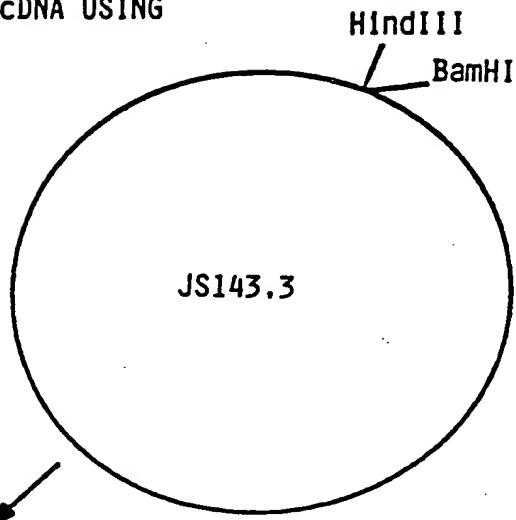


FIG. 4B

P0004344-000000000000

TOTAL RNA ISOLATED
FROM BLCL K68 CELLSSYNTHESIS OF FIRST STRAND cDNA USING
OLIGO-dT PRIMERcDNA
TEMPLATEPCR AMPLIFICATION WITH
DR1B-B & DR1B-F PRIMERSHindIII BamHI

β1-β2-HINGE PCR
PRODUCTHindIII/BamHI
DIGESTHindIII/BamHI
DIGEST

HindIII



BamHI

pB712

TEMPLATE FOR PCR
AMPLIFICATIONSPCR WITH BF-NN
& BB-S PRIMERS

NcoI

SpeI

β1-β2-HINGE
PCR PRODUCT

FIG. 5A

DRAFT - DRAFT

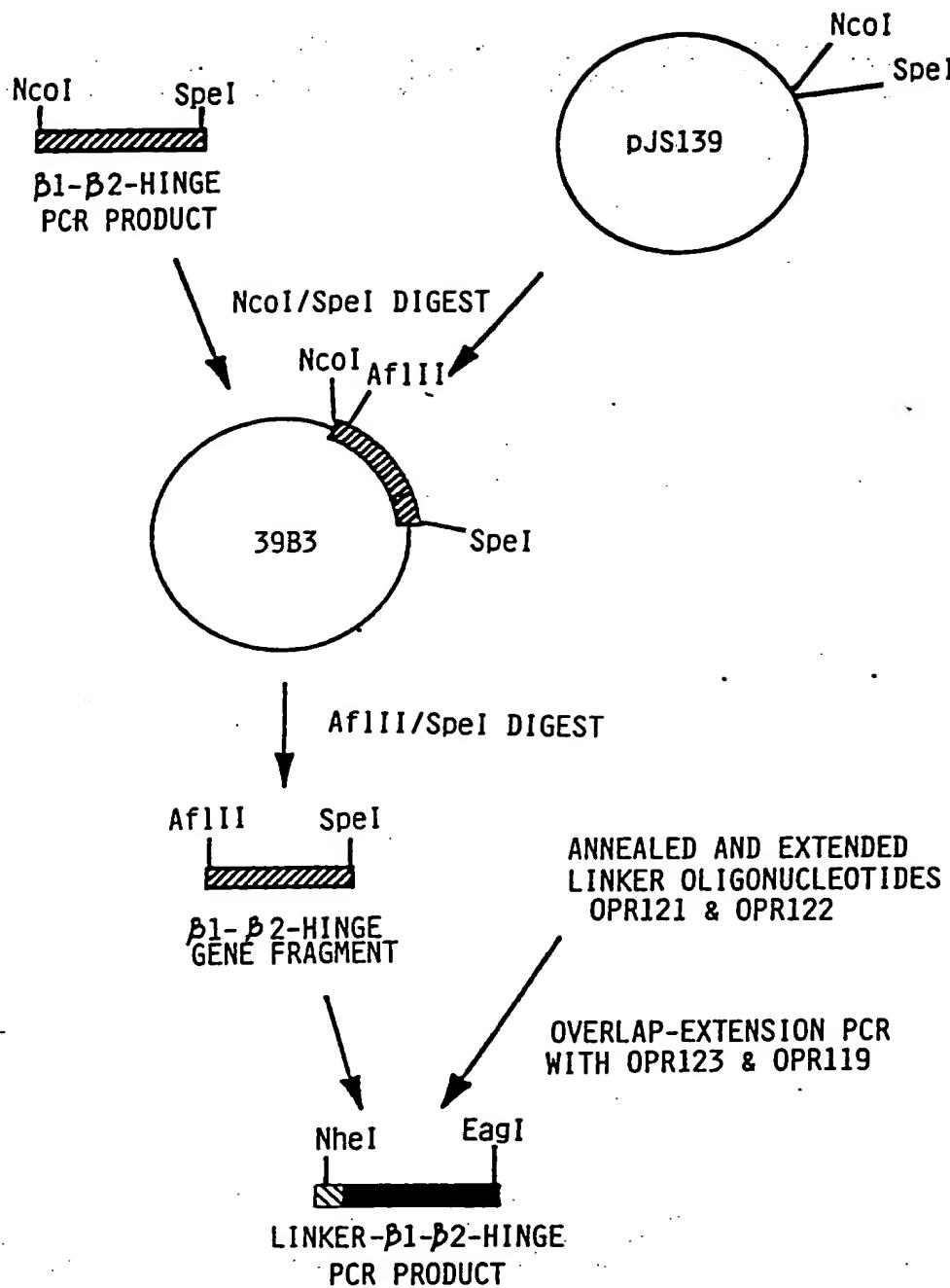
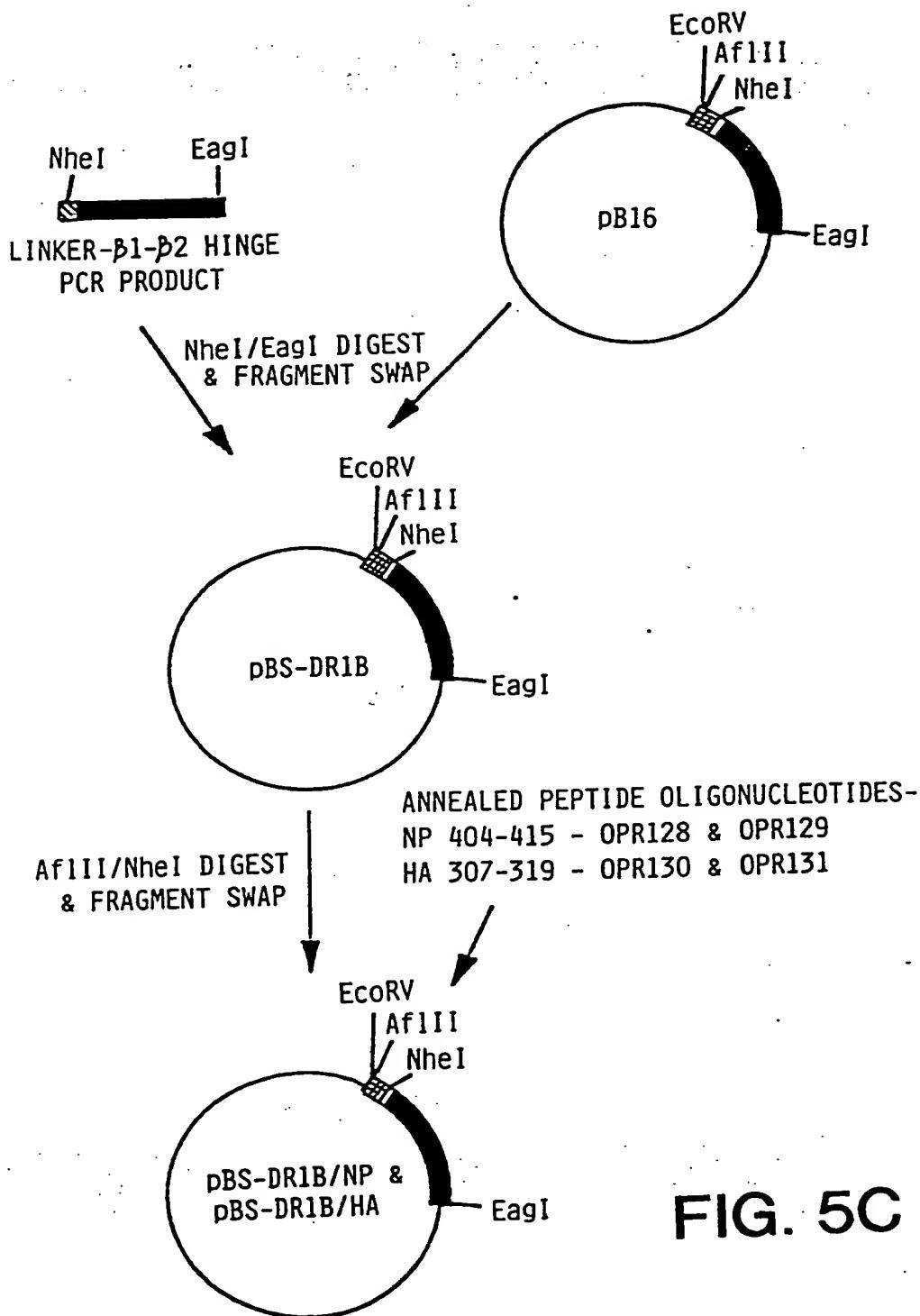


FIG. 5B

RECORDED - FEBRUARY 2000

**FIG. 5C**

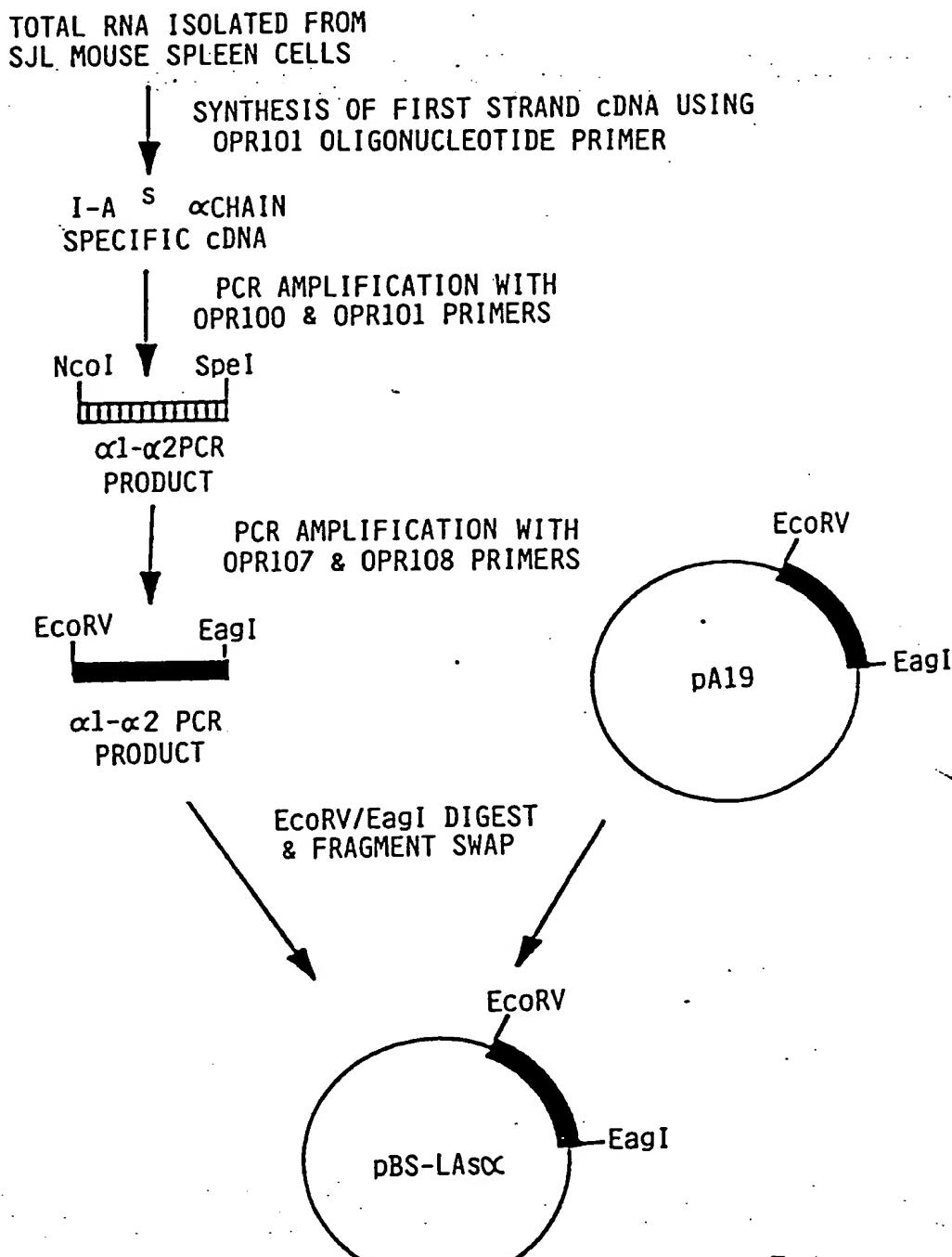
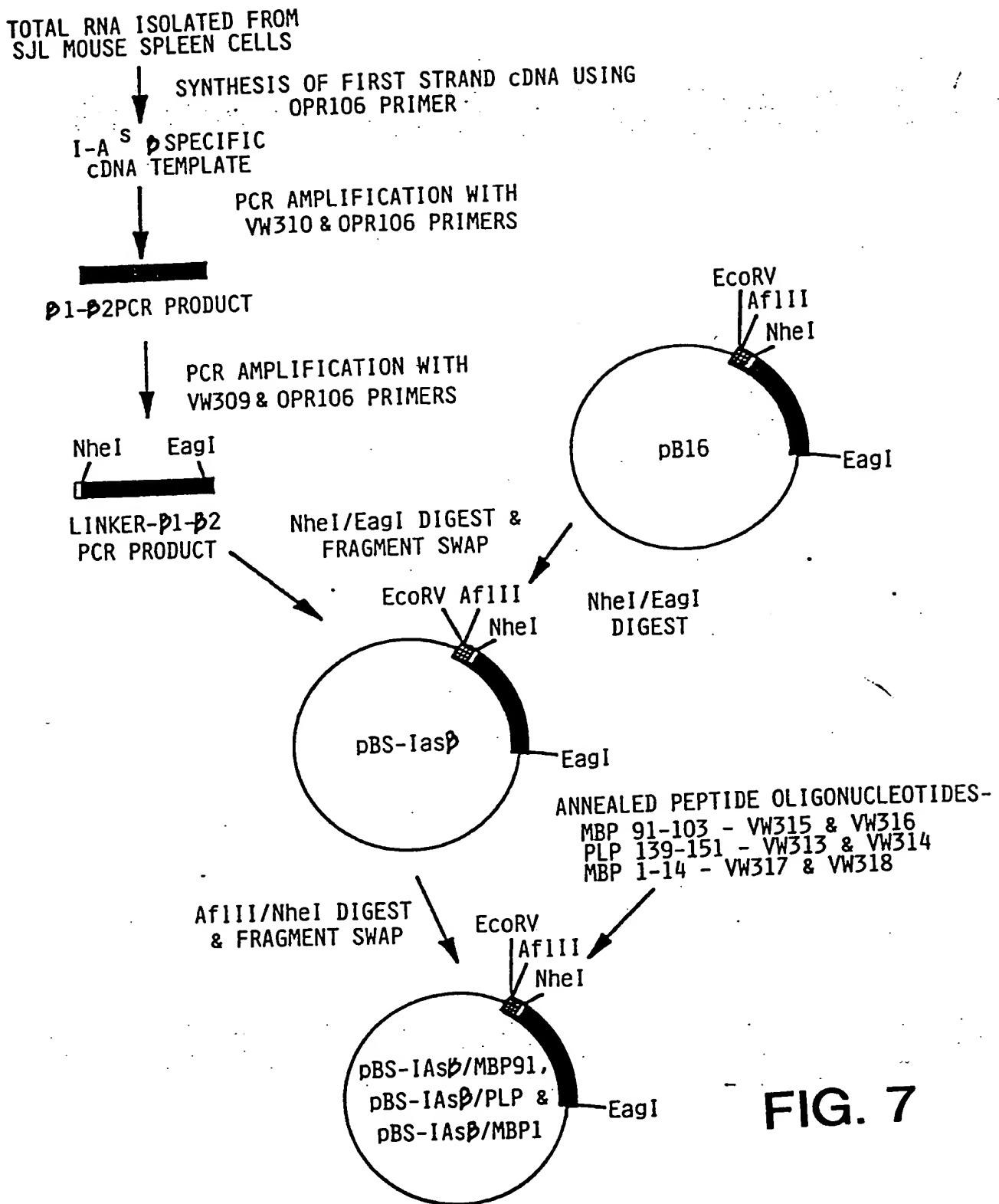


FIG. 6



I-Ad/I-As PCR PRIMERS AND CLONING OLIGONUCLEOTIDES
(RESTRICTION SITE ARE UNDERLINED).

OPR100 5'-GGG GCG ATG GCC GAA GAC GAC GAC ATT GAG GCC GAC-3'

OPR101 5'-GCG ACT AGT CCA GTG TTT CAG AAC CGG CTC-3'

OPR107 5'-CCC CCC GAT ATC TCA GCT TCC AGC AGT GGA GAC GAC ATT GAG
GCC G-3'

OPR108 5'-CCC CCC CGG CCG CTA CTT ACG TTT CCA GTG TTT CAG AAC CGG
C-3'

OPR102 5'-GGG GCG ATG GCC GGA AAC TCC GAA AGG CAT TTC G-3'

OPR104 5'-GCG GCG ACT AGT CCA CTC CAC AGT GAT GGG GC-3'

OPR106 5'-CCC CCC CGG CCG TAC CTG AGG ACC ACT CCA CAG TGA TGG-3'

OPR112 5'-CCC CCC GAT ATC ACA GGT GTC TTA AGT GCT AGC GGA GGG GGC
GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC-3'

OPR119 5'-AGC TTG ATA TCA CAG GTG TCT TAA GTG GAG-3'.

OPR120-2 5'-CTA GCT CCA CTT AAG ACA CCT GTG ATA TCA-3'

VW310 5'-TCC GGA GGC GGC GGA GAC TCC GAA AGG CAT TTC G-3'

VW309 5'-CGA TCG CTA GCG GCG GTG GTG GTT CCG GTG GCG GCG GAG-3'

OPR136 5'-CCC CCC AGG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC
TG-3'

OPR139 5'-CCC CCC GAG CTC GAA TTC TCA TAA AGG CCC TGG GTG TCT G-3'

OPR132 5'-CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA
GC-3'

OPR133 5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134 5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135 5'-CCC CCC GAG CTC GAA TTC TCA CTG CAG GAG CCC TGC TGG-3'

FIG. 8A

HLA-DRI PCR PRIMERS AND CLONING OLIGONUCLEOTIDES.

DRIA-F
5'-GGG GGG AAG CTT ATG ATC AAA GAA GAA CAT GTG ATC ATC-3'DRIA-B
5'-GCG GCG GGA TCC GTT CTC TGT AGT CTC TGG GAG AGG-3'DRIB-F
5'-GGG GGG AAG CTT ATG GGG GAC ACC CGA CCA CGT TTC TTG TGG
CAG C-3'AF-N
5'-GGG GGG GCC ATG GCC ATC AAA GAA GAA CAT GTG ATC ATC-3'AB-S
5'-GCG GCG ACT AGT GTT CTC TGT AGT CTC TGG GAG AGG-3'OPR124
5'-GGG GGG AAG CTT GAT ATC TCA GCT TCC AGC AGT AGT ATC AAA
GAA GAA CAT GTG ATC-3'OPR125
5'-GGG GGG CGG CCG CTA CTT ACG TTT CTC TGG GAG AGG GCT TGG
AGC-3'DRIB-B
5'-GCG GCG GGA TCC CTT GCT CTG TGC AGA TTC AGA CC-3'BF-NN
5'-GGG GGG GCC ATG GCC GGA TCC GCT AGC GGG GAC ACC CGA CCA
CGT TTC TTG-3'BB-S
5'-GCG GCG ACT AGT CTT GCT CTG TGC AGA TTC AGA CCG-3'OPR121
5'-GTT GTC TTA AGT GGA GCT AGC GGA GGG GGC GGG TCC GGA GGT
GGT GGG GAC ACC CG-3'OPR122
5'-GAA ATG ACA TTC AAA CTT CAG CTG CCA CAA GAA ACG TGG TCG
GGT GTC CCC ACC ACC-3'OPR123
5'-GGG GGG CGG CCG TAC CTG AGG ACT TGC TCT GTG CAG ATT CAG-
3'

FIG. 8B

PEPTIDE OLIGONUCLEOTIDES.

Ova 323-339

OPR110
5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC GCT GAA ATC
AAC GAA GCT GGT CGT G-3'OPR111
5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC TGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

Ova H331R

OPR115
5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CGG GCT GAA ATC
AAC GAA GCT GGT CGT G-3'OPR116
5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC CGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

Ova A332Y

OPR117
5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC TAC GAA ATC
AAC GAA GCT GGT CGT G-3'OPR116
5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA TAG TGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

HEL 74-86

OPR140
5'-TTA AGT AAC CTG TGC AAC ATC CCC TGC AGC GCC CTG CTG AGC
TCC G-3'OPR141
5'-CTA GCG GAG CTC AGC AGG GCG CTG CAG GGG ATG TTG CAC AGG
TTA C-3'

NP 404-415

OPR128
5'-TTA AGT CAG ATC AGC GTG CAG CCC GCC TTC AGC GTG CAG G-3'

FIG. 8C

OPR129
 5'-CTA GCC TGC ACG CTG AAG GCG GGC TGA ACG CTG ATC TGA C-3'

HA 307-319

OPR130
 5'-TTA AGT CCC AAG TAC GTG AAG CAG AAC ACC CTG AAG CTG GCC
 ACC G-3'

OPR131
 5'-CTA GCG GTG GCC AGC TTC AGG GTG TTC TGC TTC ACG TAC TTG
 GGA C-3'

MBP 91-103

VW315
 5'-TTA AGT CAC TAT GGC TCC CTG CCG CAG AAG TCC CAG CAC GGG
 CGC G-3'

VW316
 5'-CTA GCG CGC CCG TGC TGG GAC TTC TGC GGC AGG GAG CCA TAG
 TGA C-3'

PLP 139-151

VW313
 5'-TTA CAT CAC TCC CTG GGC AAG TGG CTG GGC CAC CCG GAC AAG
 TTC G-3'

VW314
 5'-CTA GCG AAC TTG TTC GGG TGG CCC AGC CAC TTG CCC AGG GAG
 TGA C-3'

MBP 1-14

VW317
 5'-TTA AGT ATG GCA TCC CAG AAG CGC CCG TCC CAG CGC TCC AAG
 TAC CTG G-3'

VW316
 5'-CTA GCC AGG TAC TTG GAG CGC TGG GAC GGG CGC TTC TGG GAT
 GCC ATA C-3'

FIG. 8D

FIG. 9A

RESTRICTION SITES FOR INSERTION OF OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST

Af III		Nhe I		LINKER REGION		I-Ad β CHAIN	
ECORV	10	20	30	40	50	60	70
GATATCACAGGT	GTC TTA AGT	GGA GCT	GGA CCT	GGA CCT	GGA CCT	TCC AGG	AGG CAT
CTATAGTGTCCA	CAG AAT TCA	CGA TCG	CCC CCT	CCC CCT	CCC CCT	CTT AGG	CTT GTA
V	L	S	G	G	G	N	H
196 H CHAIN INTRON		SIGNAL PEPTIDE CLEAVAGE SITE					

xbar

I-Ad β CHAIN 196 H CHAIN INTRON

FIG. 9B

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ECORV 10 20 30 40 50 550 560 570 580
 TCC AGC AGT GAA GAC ATT GAG GCC GAC CAC TGG AAA CGT AAGTAGGGGGCTG
 TCG TCA CTT GCT CGG TAA CTC GCA GAC TTT GTG ACC TTT GCA TTCAATGCCGGC
 AGG S D I E A D H P V L K H W K R
 CTATAGAGTCGA S S E E +1
 196 κ CHAIN SIGNAL PEPTIDE
 INTRON CLEAVAGE SITE
 196 κ CHAIN
 INTRON
 XbaI
 aai182]

FIG. 9C

RESTRICTION SITES FOR INSERTION OF OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST

ECONOMIC AFFAIRS

610 ACT GAG TGG TCC TCA 630
 ATC ACT GAG TGG TCC TCA
 TAG TGA CAC CTC ACC AGG AGT
 T V E W S S
 I -AS β CHAIN aa189 | IgG H CHAIN
 INTRON

FIG. 9D

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—

FIG. 9

RESTRICTION SITES FOR INSERTION OF OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST

ECORV	Af111		NheI	LINKER REGION
	10	20		
GATATCACAGGT	GTC	TTA	AGT	60
CTATAGTGTCCA	CAG	AAT	CCT	70
	V		66A	CGT
			30	GGA
			40	GGA
			50	GGG
			60	GGT
			70	GCA
			80	CCA
			90	CTG
			100	ACC
			110	GCT
			120	GCA
			130	TGG
			140	CGT
			150	GGT
			160	GCA
			170	AAG
			180	TTC
			190	CCT
			200	CCC
			210	CCG
			220	CGC
			230	CCT
			240	AAG
			250	GGG
			260	GGG
			270	GGT
			280	GCA
			290	CCA
			300	CTG
			310	ACC
			320	GCT
			330	GCA
			340	TGG
			350	CGT
			360	GGT
			370	GCA
			380	AAG
			390	TTC
			400	CCT
			410	CCC
			420	CCG
			430	CGC
			440	CCT
			450	AAG
			460	GGG
			470	GGG
			480	GGT
			490	GCA
			500	CCA
			510	CTG
			520	ACC
			530	GCT
			540	GCA
			550	TGG
			560	CGT
			570	GGT
			580	GCA
			590	AAG
			600	TTC
			610	CCT
			620	CCC
			630	CCG
			640	CGC
			650	CCT
			660	AAG
			670	GGG
			680	GGG
			690	GGT
			700	GCA
			710	CCA
			720	CTG
			730	ACC
			740	GCT
			750	GCA
			760	TGG
			770	CGT
			780	GGT
			790	GCA
			800	AAG
			810	TTC
			820	CCT
			830	CCC
			840	CCG
			850	CGC
			860	CCT
			870	AAG
			880	GGG
			890	GGG
			900	GGT
			910	GCA
			920	CCA
			930	CTG
			940	ACC
			950	GCT
			960	GCA
			970	TGG
			980	CGT
			990	GGT
			1000	GCA
			1010	AAG
			1020	TTC
			1030	CCT
			1040	CCC
			1050	CCG
			1060	CGC
			1070	CCT
			1080	AAG
			1090	GGG
			1100	GGG
			1110	GGT
			1120	GCA
			1130	CCA
			1140	CTG
			1150	ACC
			1160	GCT
			1170	GCA
			1180	TGG
			1190	CGT
			1200	GGT
			1210	GCA
			1220	AAG
			1230	TTC
			1240	CCT
			1250	CCC
			1260	CCG
			1270	CGC
			1280	CCT
			1290	AAG
			1300	GGG
			1310	GGG
			1320	GGT
			1330	GCA
			1340	CCA
			1350	CTG
			1360	ACC
			1370	GCT
			1380	GCA
			1390	TGG
			1400	CGT
			1410	GGT
			1420	GCA
			1430	AAG
			1440	TTC
			1450	CCT
			1460	CCC
			1470	CCG
			1480	CGC
			1490	CCT
			1500	AAG
			1510	GGG
			1520	GGG
			1530	GGT
			1540	GCA
			1550	CCA
			1560	CTG
			1570	ACC
			1580	GCT
			1590	GCA
			1600	TGG
			1610	CGT
			1620	GGT
			1630	GCA
			1640	AAG
			1650	TTC
			1660	CCT
			1670	CCC
			1680	CCG
			1690	CGC
			1700	CCT
			1710	AAG
			1720	GGG
			1730	GGG
			1740	GGT
			1750	GCA
			1760	CCA
			1770	CTG
			1780	ACC
			1790	GCT
			1800	GCA
			1810	TGG
			1820	CGT
			1830	GGT
			1840	GCA
			1850	AAG
			1860	TTC
			1870	CCT
			1880	CCC
			1890	CCG
			1900	CGC
			1910	CCT
			1920	AAG
			1930	GGG
			1940	GGG
			1950	GGT
			1960	GCA
			1970	CCA
			1980	CTG
			1990	ACC
			2000	GCT
			2010	GCA
			2020	TGG
			2030	CGT
			2040	GGT
			2050	GCA
			2060	AAG
			2070	TTC
			2080	CCT
			2090	CCC
			2100	CCG
			2110	CGC
			2120	CCT
			2130	AAG
			2140	GGG
			2150	GGG
			2160	GGT
			2170	GCA
			2180	CCA
			2190	CTG
			2200	ACC
			2210	GCT
			2220	GCA
			2230	TGG
			2240	CGT
			2250	GGT
			2260	GCA
			2270	AAG
			2280	TTC
			2290	CCT
			2300	CCC
			2310	CCG
			2320	CGC
			2330	CCT
			2340	AAG
			2350	GGG
			2360	GGG
			2370	GGT
			2380	GCA
			2390	CCA
			2400	CTG
			2410	ACC
			2420	GCT
			2430	GCA
			2440	TGG
			2450	CGT
			2460	GGT
			2470	GCA
			2480	AAG
			2490	TTC
			2500	CCT
			2510	CCC
			2520	CCG
			2530	CGC
			2540	CCT
			2550	AAG
			2560	GGG
			2570	GGG
			2580	GGT
			2590	GCA
			2600	CCA
			2610	CTG
			2620	ACC
			2630	GCT
			2640	GCA
			2650	TGG
			2660	CGT
			2670	GGT
			2680	GCA
			2690	AAG
			2700	TTC
			2710	CCT
			2720	CCC
			2730	CCG
			2740	CGC
			2750	CCT
			2760	AAG
			2770	GGG
			2780	GGG
			2790	GGT
			2800	GCA
			2810	CCA
			2820	CTG
			2830	ACC
			2840	GCT
			2850	GCA
			2860	TGG
			2870	CGT
			2880	GGT
			2890	GCA
			2900	AAG
			2910	TTC
			2920	CCT
			2930	CCC
			2940	CCG
			2950	CGC
			2960	CCT
			2970	AAG
			2980	GGG
			2990	GGG
			3000	GGT
			3010	GCA
			3020	CCA
			3030	CTG
			3040	ACC
			3050	GCT
			3060	GCA
			3070	TGG
			3080	CGT
			3090	GGT
			3100	GCA
			3110	AAG
			3120	TTC
			3130	CCT
			3140	CCC
			3150	CCG
			3160	CGC
			3170	CCT
			3180	AAG
			3190	GGG
			3200	GGG
			3210	GGT
			3220	GCA
			3230	CCA
			3240	CTG
			3250	ACC
			3260	GCT
			3270	GCA
			3280	TGG
			3290	CGT
			3300	GGT
			3310	GCA
			3320	AAG
			3330	TTC
			3340	CCT
			3350	CCC
			3360	CCG
			3370	CGC
			3380	CCT
			3390	AAG
			3400	GGG
			3410	GGG
			3420	GGT
			3430	GCA
			3440	CCA
			3450	CTG
			3460	ACC
			3470	GCT
			3480	GCA
			3490	TGG
			3500	CGT
			3510	GGT
			3520	GCA
			3530	AAG
			3540	TTC
			3550	CCT
			3560	CCC
			3570	CCG
			3580	CGC
			3590	CCT
			3600	AAG
			3610	GGG
			3620	GGG
			3630	GGT
			3640	GCA
			3650	CCA
			3660	CTG
			3670	ACC
			3680	GCT
			3690	GCA
			3700	TGG
			3710	CGT
			3720	GGT
			3730	GCA
			3740	AAG
			3750	TTC
			3760	CCT
			3770	CCC
			3780	CCG
			3790	CGC
			3800	CCT
			3810	AAG
			3820	GGG
			38	

DR-1 β CHAIN

IgG H CHAIN
Intron

FIG. 9E

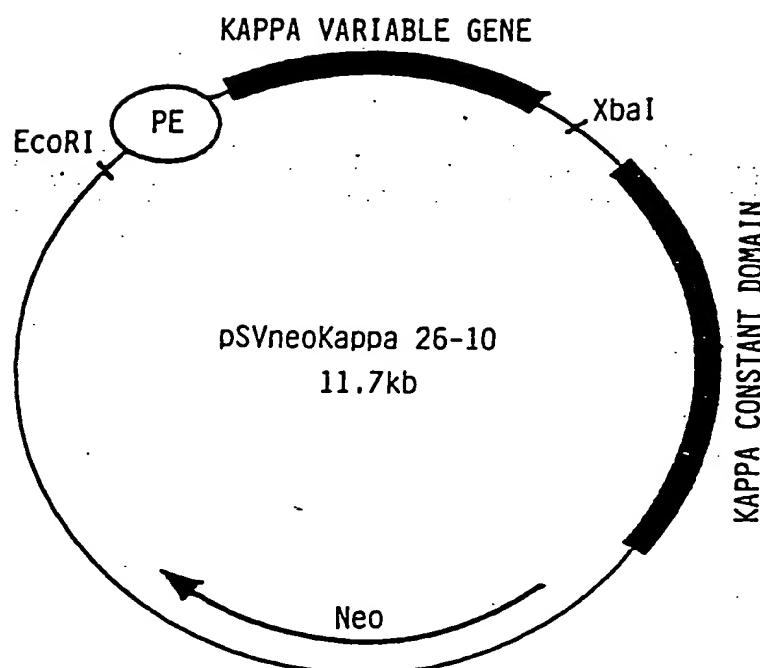


FIG. 10A

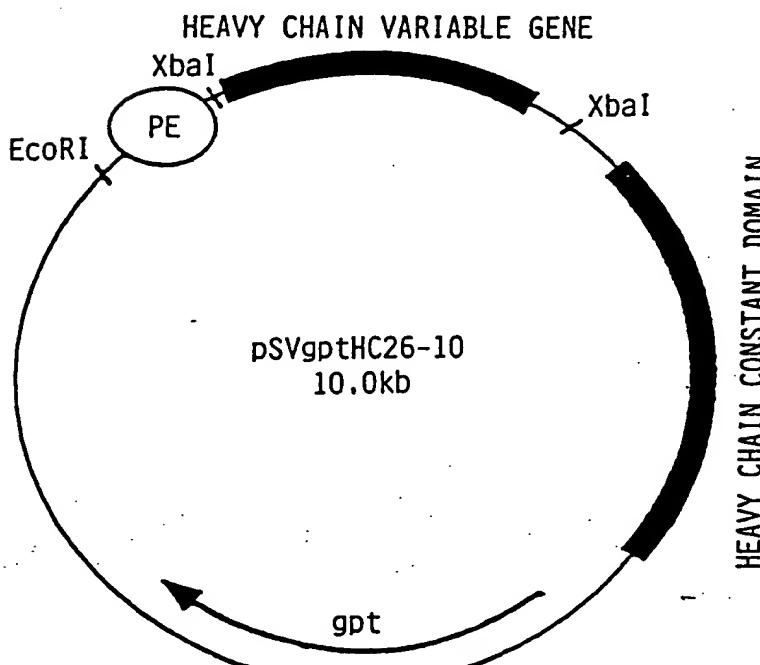


FIG. 10B

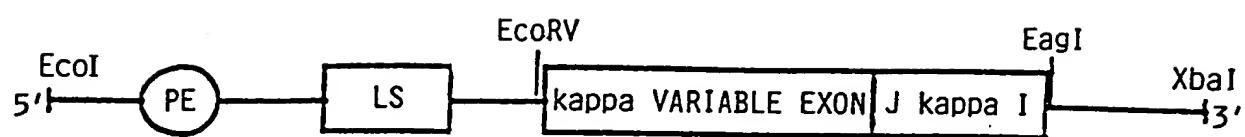


FIG. 11A



FIG. 11B

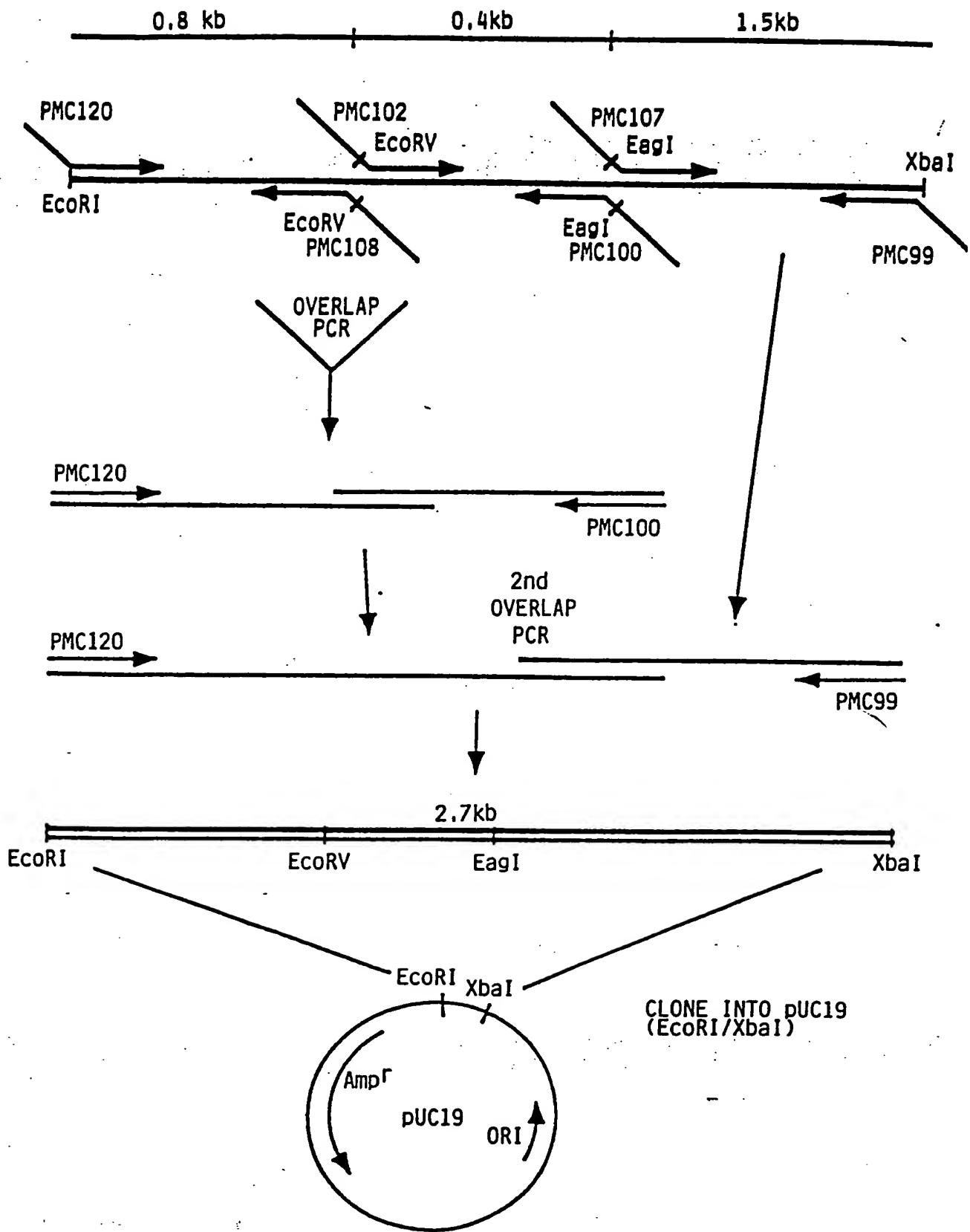


FIG. 12

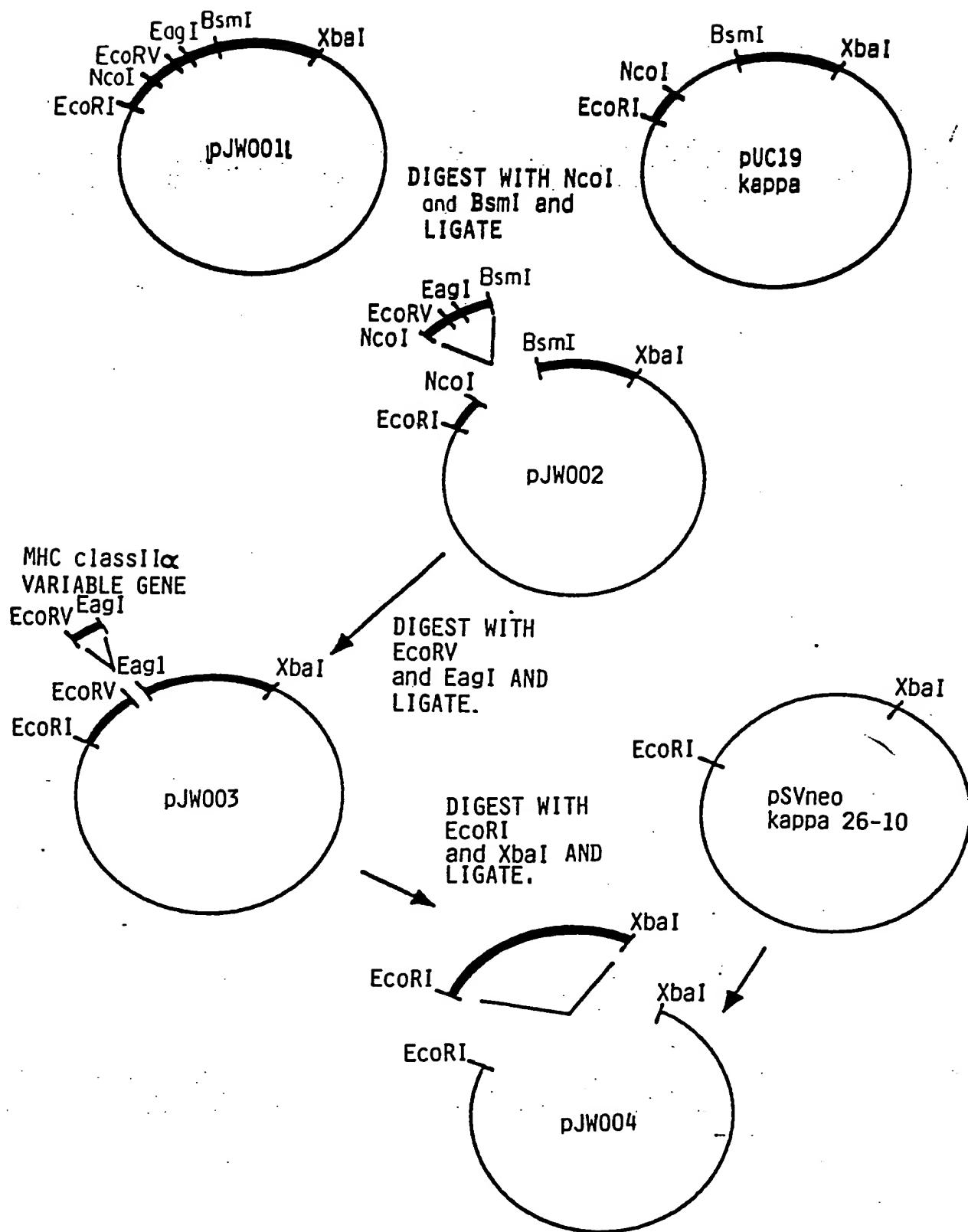


FIG. 13

PRIMER LIST

PMC-33

[5'GCTCAGCTGTCTTGTTCAGTACTGATC3']

PMC-77

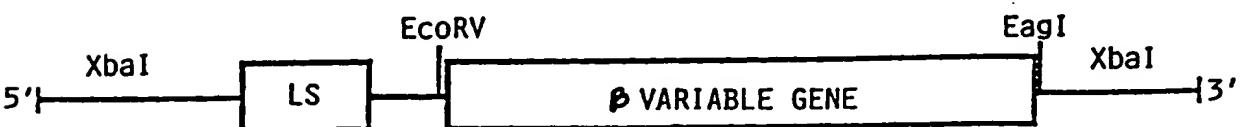
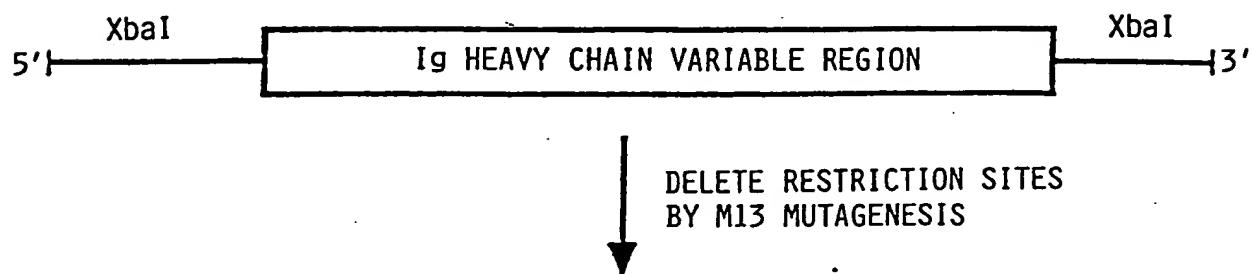
[5'GTAAGTAGCGGCCG3']

PMC-111

[5'GGTATGTAAAAATAAACATCACAG3']

PMC-114

[5'GCTTGCTTACGGAGTTACTC3']

SEQUENCE**FIG. 14****FIG. 15**

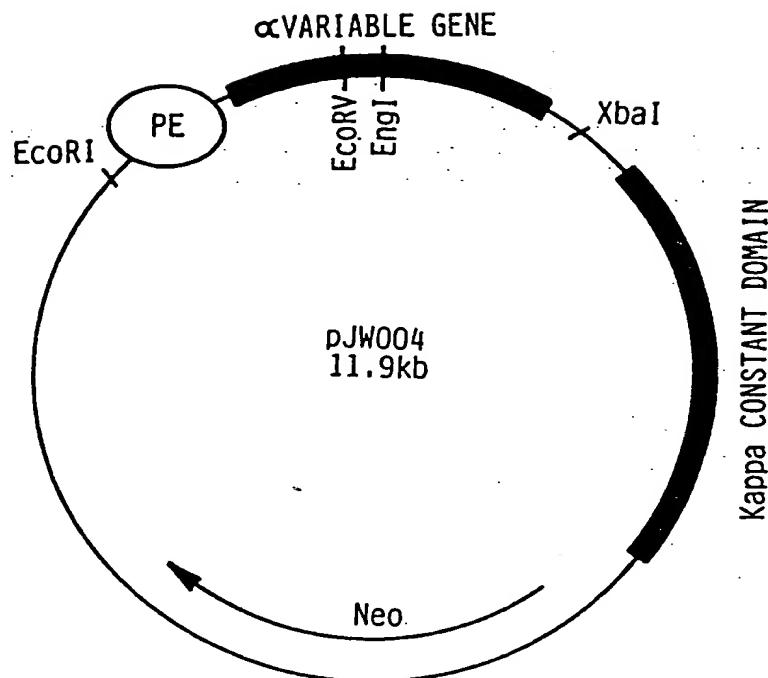


FIG. 16A

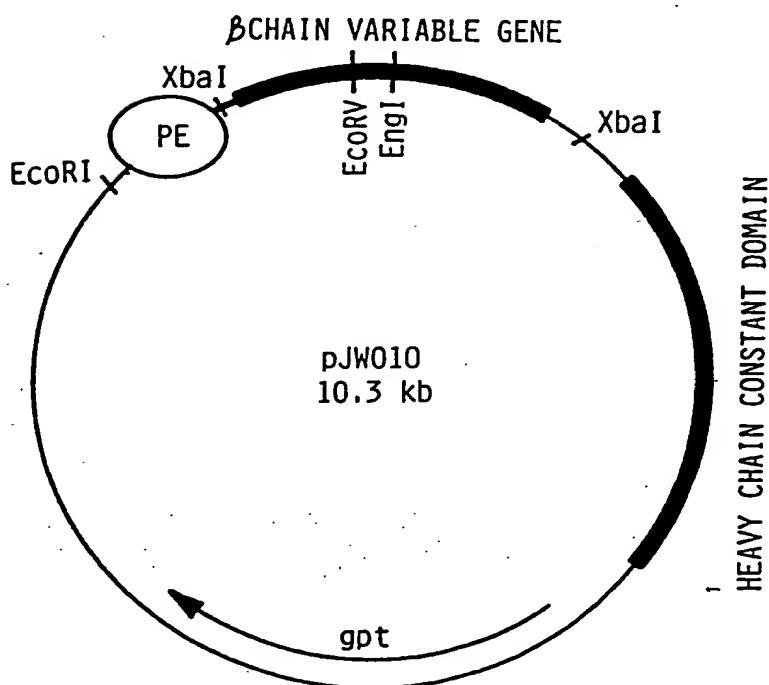


FIG. 16B

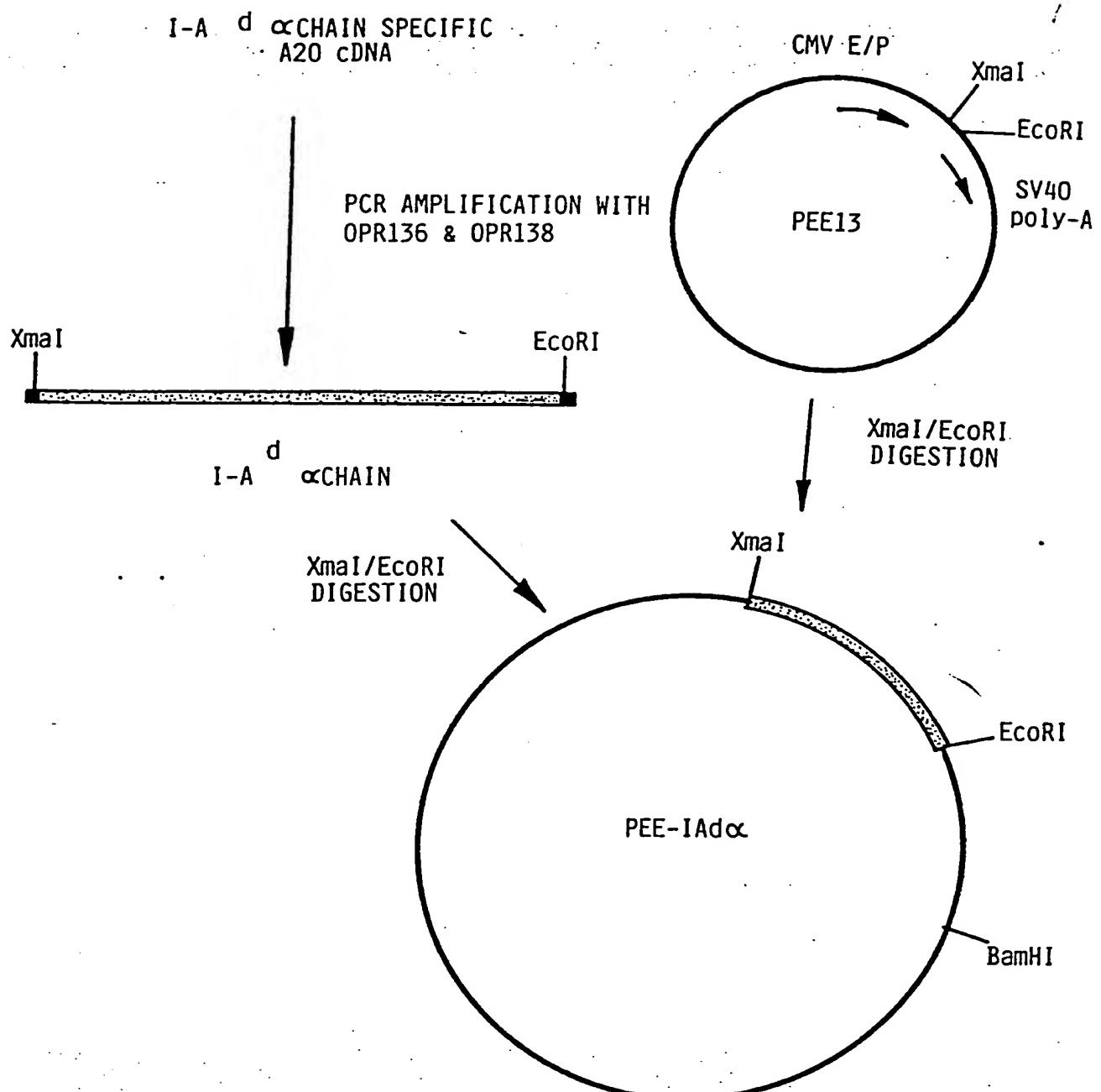
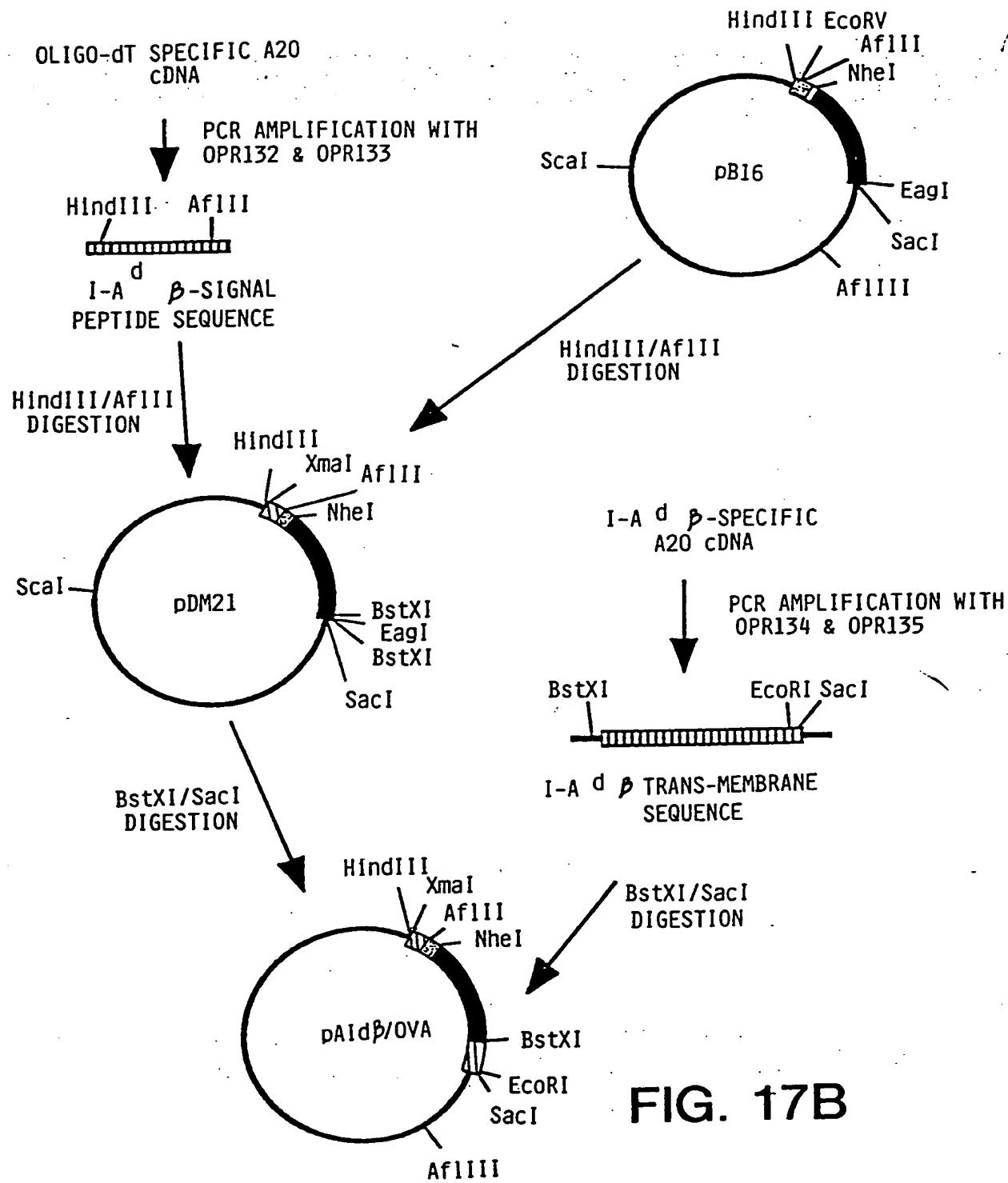


FIG. 17A

RECEIVED: FEBRUARY 1989



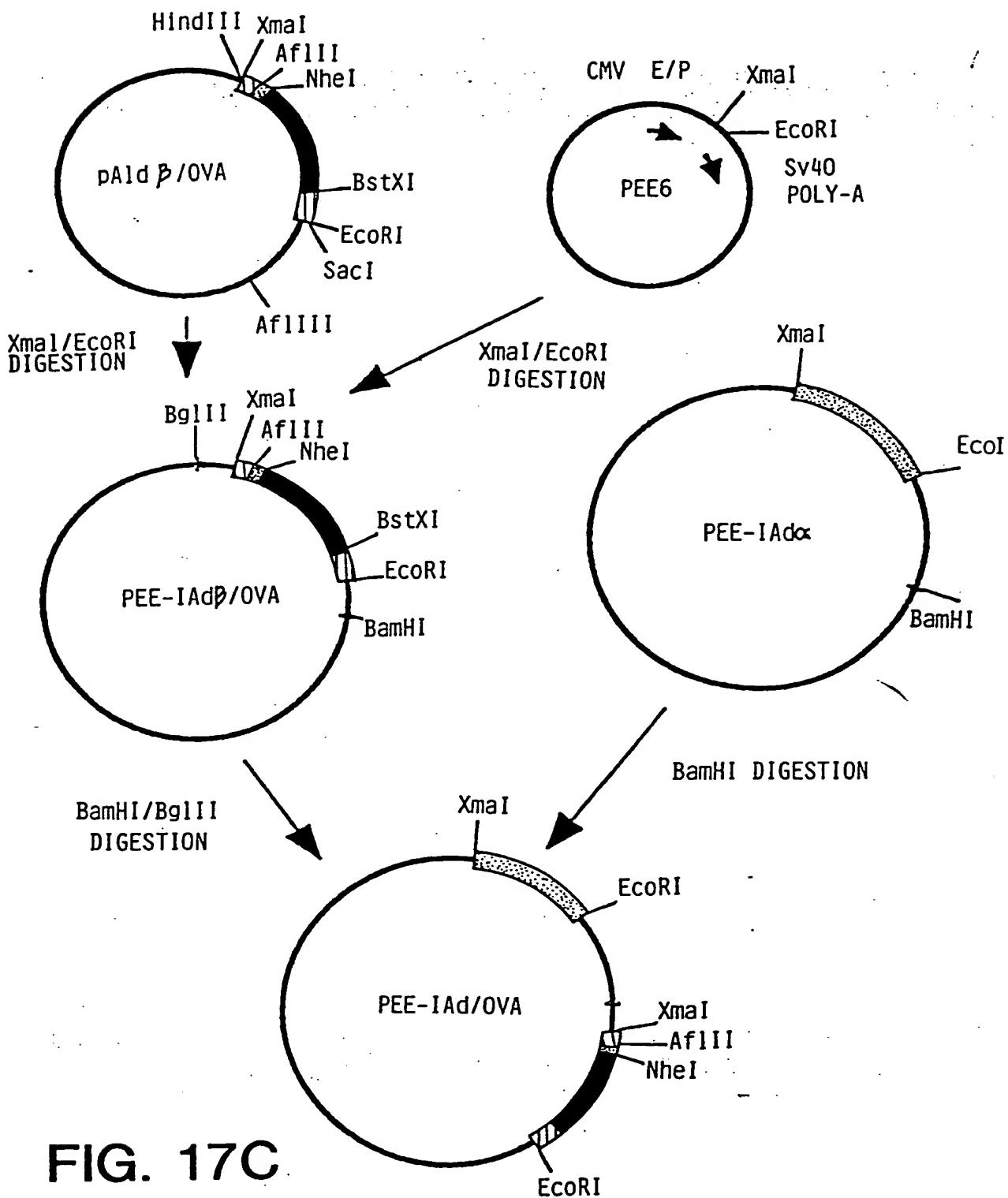


FIG. 17C

XbaI

10	C	ATG	CCG	TGC	AGC	AGA	GCT	CTG	ATT	CTG	40	GTC	CTC	GCC
GGGCCC GG TG	G	TAC	GGC	ACG	TCG	TCT	CGA	GAC	TAA	GAC	CCC	CAG	GAG	CGG
	M	P	C	S	R	A	L	I	L	G	V	L	A	

I-Ad^d α CHAIN SIGNAL PEPTIDE

KOZAK
CONSENSUS

60	CTG	AAC	ACC	ATG	CTC	AGC	CTC	TGC	GGA	GGT	80	GAA	GAC	GAC	90
GAC	TTG	TGG	TAC	GAG	TCG	GAG	ACG	CCT	CCA	CTT	CTG	CTG	TAA	CTC	//
L	N	T	M	L	S	L	C	G	G	E	D	D	I	E	//

+1

I-Ad^d α CHAIN SIGNAL PEPTIDE SIGNAL PEPTIDE
CLEAVAGE SITE

EcoRI

750	CGA	TCA	GGT	GGC	ACC	760	TCC	AGA	CAC	770	CCA	GGG	CCT	780	TGA	GAATT
GCT	AGT	CCA	CCG	TGG	AGG	TCT	R	GTG	GGT	CCC	GGA	AAT	ACT	*	CTTAAG	
R	S	G	G	T	S	R	H	P	G	P	L			STOP		

I-Ad^d α CHAIN

FIG. 18A

HindIII XbaI

AAGCTTCCCG	GGCCACC	ATG	GCT	CTG	CAG	ATC	CCC	AGC	CTC	CTC	CTC	TCA	GCT
TTCGAAGGGC	CCGGTGG	TAC	CGA	GAC	GTC	TAG	GGG	TCG	GAG	GAG	GAG	ACT	CGA
M	A	L	Q	I	P	S	L	L	L	L	S	A	

KOZAK
CONSENSUSI-A^d β CHAIN SIGNAL PEPTIDE

AflII

GCT	GTG	GTG	GTG	CTG	ATG	GTG	CTG	AGC	AGC	CCA	AGG	ACC	TTA	AGT	ATC
CGA	CAC	CAC	CAC	GAC	TAC	CAC	GAC	TCG	TCG	GGT	TCC	TGG	AAT	TCA	TAG
A	V	V	V	L	M	V	L	S	S	P	R	T	L	S	I

I-A^d β CHAIN SIGNAL PEPTIDESIGNAL PEPTIDE
CLEAVAGE SITE

TCT	CAG	GCT	GTT	CAC	GCT	120	CAC	GCT	130	GAA	ATC	AAC	GAA	140	GCT	GGT	CGT
AGA	GTC	CGA	CAA	GTG	CGA	CGA	GTG	CGA	CTT	ATC	TTG	CTT	CGA	CCA	GCA		
S	Q	A	V	H	A	A	H	A	E	I	N	E	A	G	R		

Ova PEPTIDE

NheI

150	GCT	AGC	GGA	GGG	GGC	GGA	160	AGC	GGC	GGA	170	GGA	GGG	180	GGA	190	GAA	AGG	//
CGA	TCG	CCT	CCC	CCG	CCT	TCG	S	CGA	CCG	CCT	G	G	G	CCT	CTT	CTT	TCC	TCC	//
A	S	G	G	G	G	S	G	A	G	CCG	N	N	S	TTG	E	R	AGG	AGG	//

LINKER REGION

I-A^d β CHAIN

EcoRI SacI

870	CCT	CCT	CCA	880	GCA	GGG	CTC	890	CTG	CAG	TGA	900	GAAT	TCGAGCTC	
GGA	GGA	GGT	CGT	CCC	GAG	L	L	Q	GAC	GTC	ACT	CTTA	AGCTCGAG		
P	P	P	A	G					*						

STOP

I-A^d β CHAIN

FIG. 18B

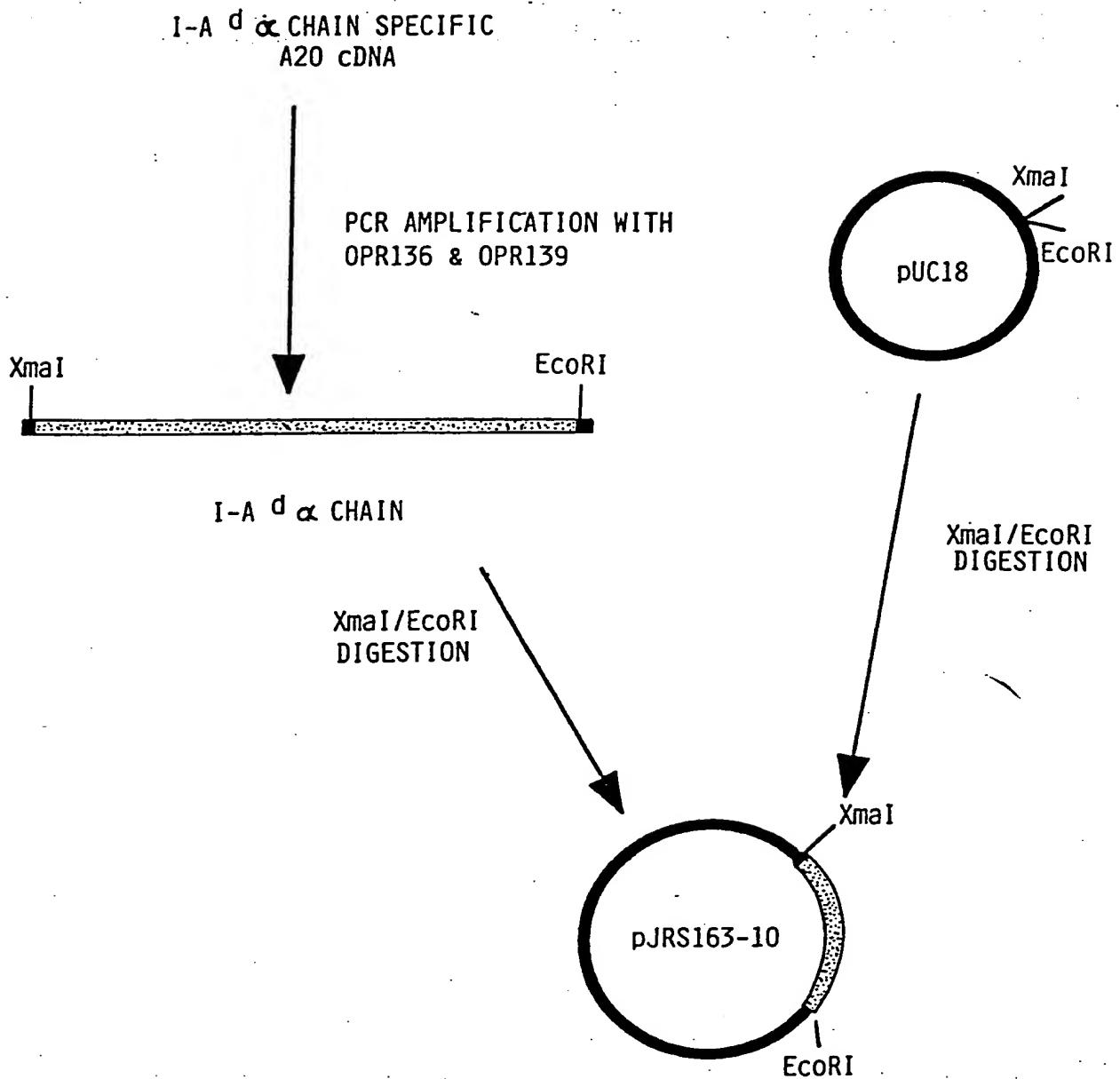


FIG. 19A

0881474 050202

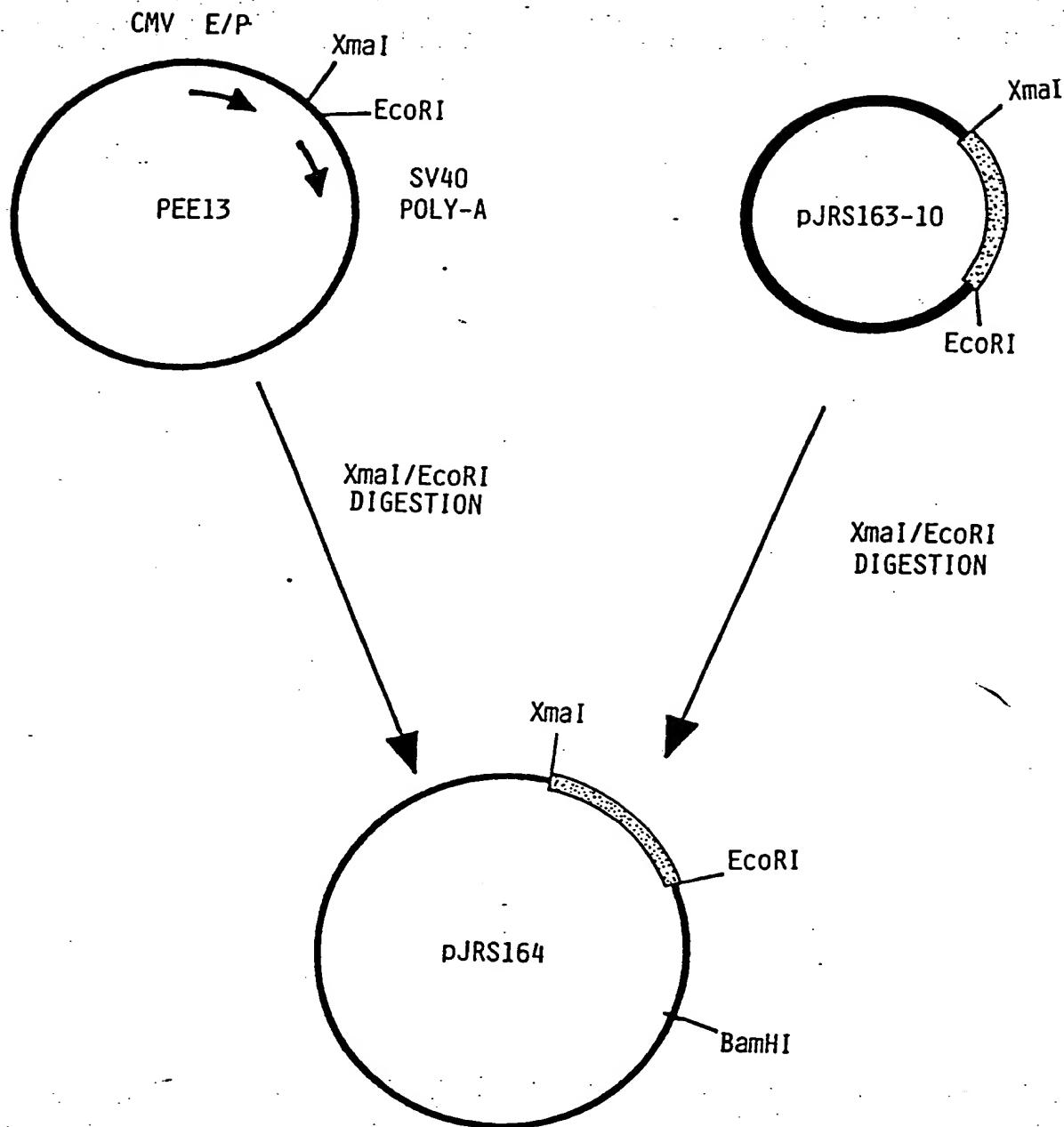
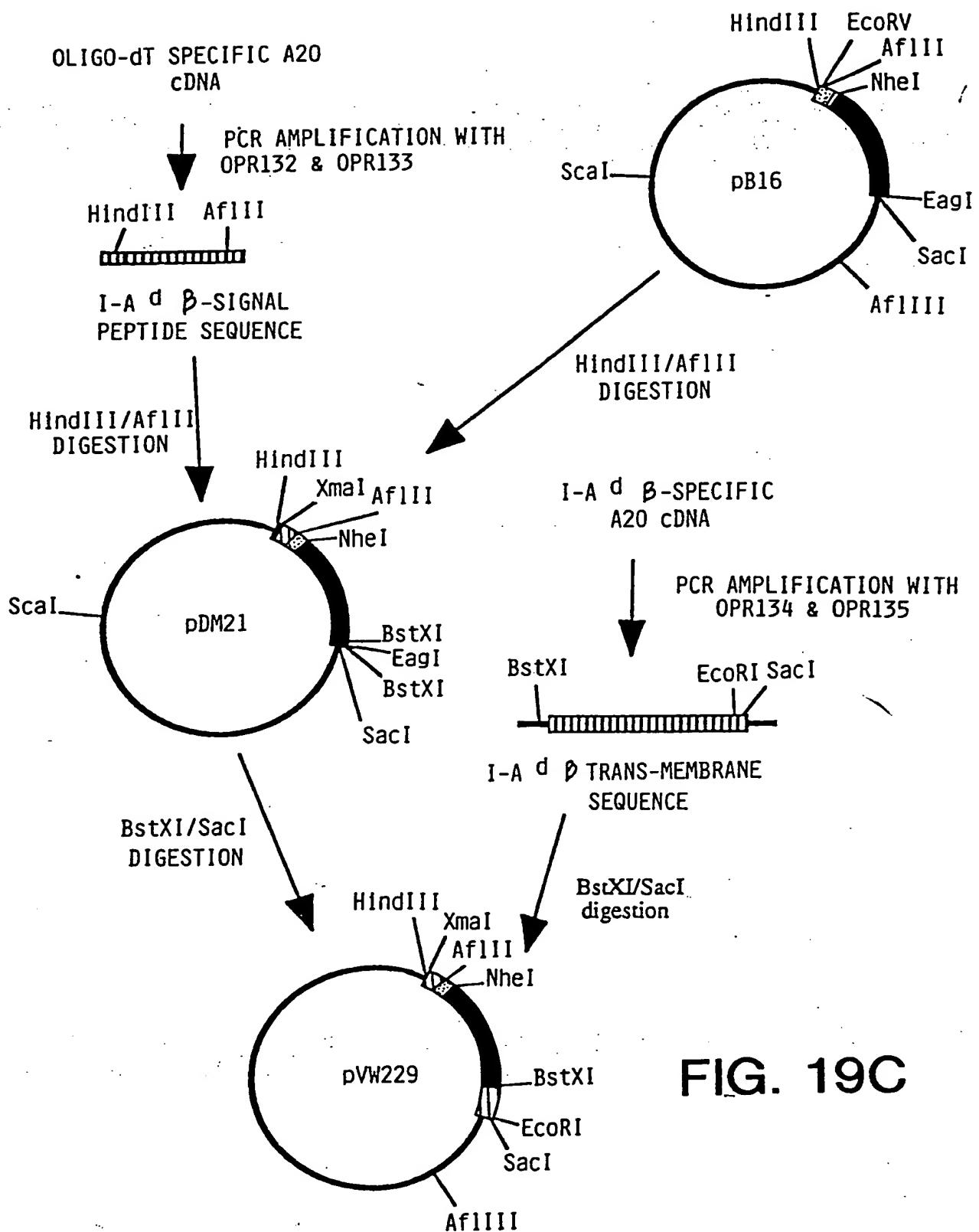


FIG. 19B



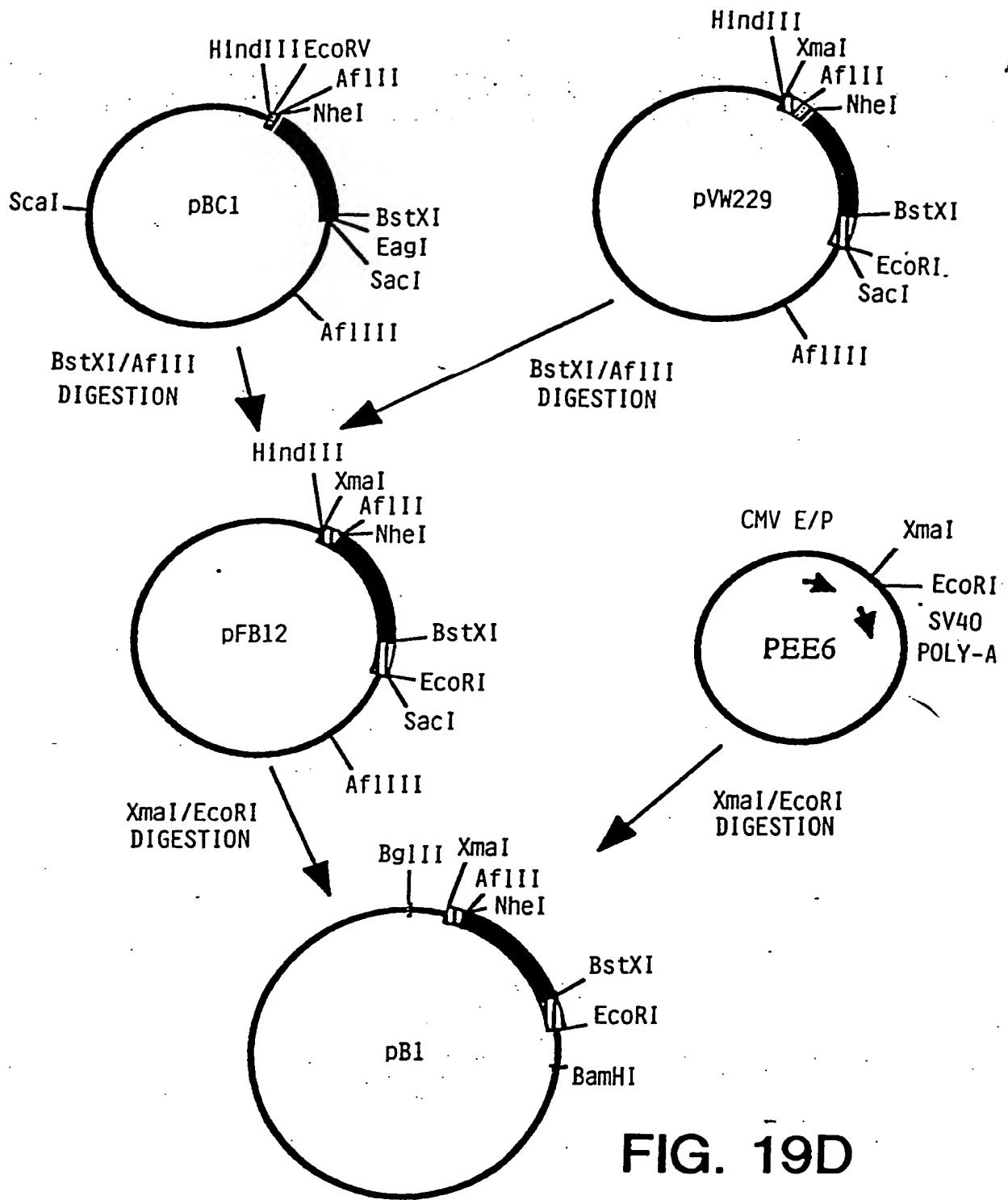


FIG. 19D

0981947 - 050302

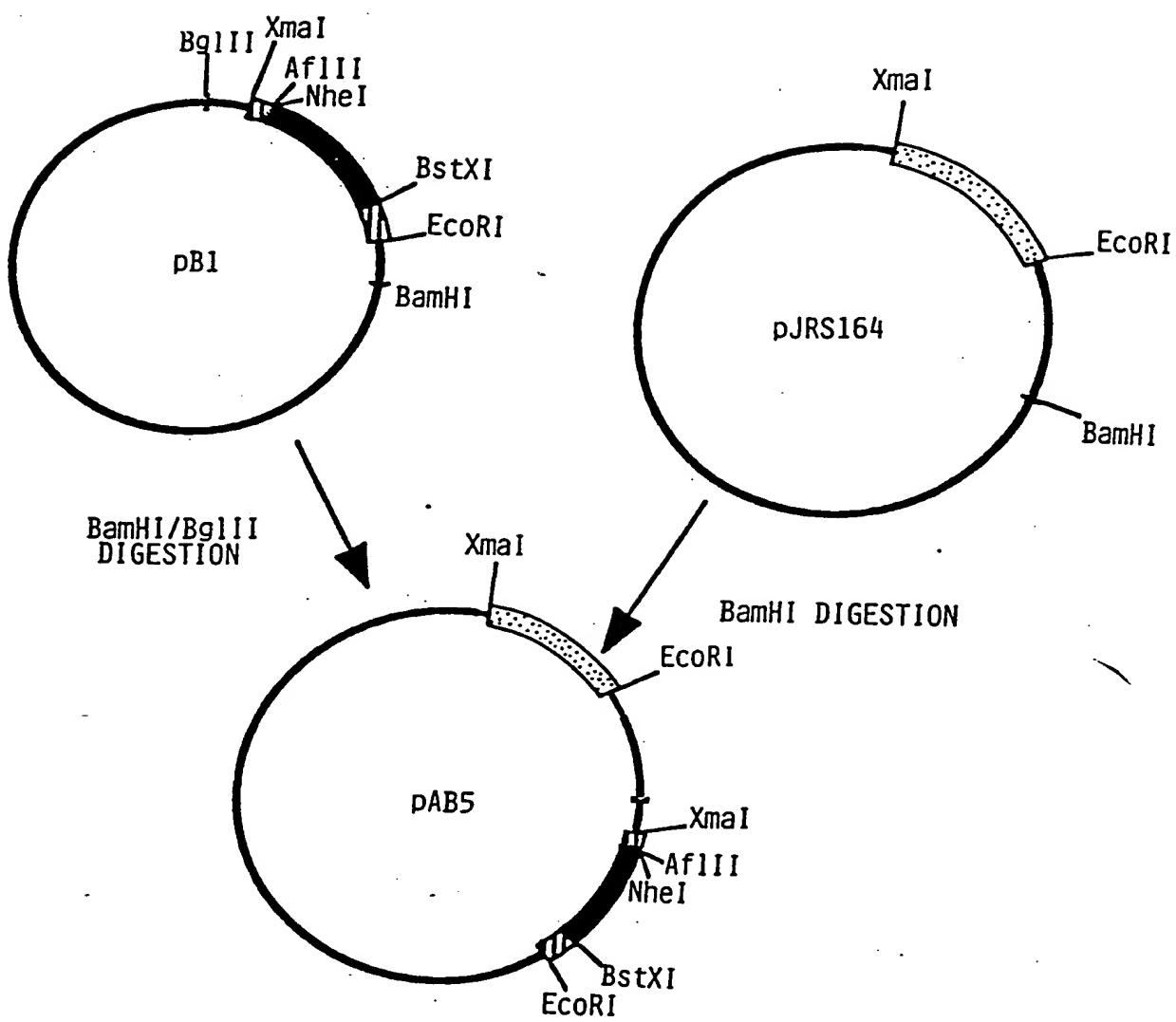


FIG. 19E

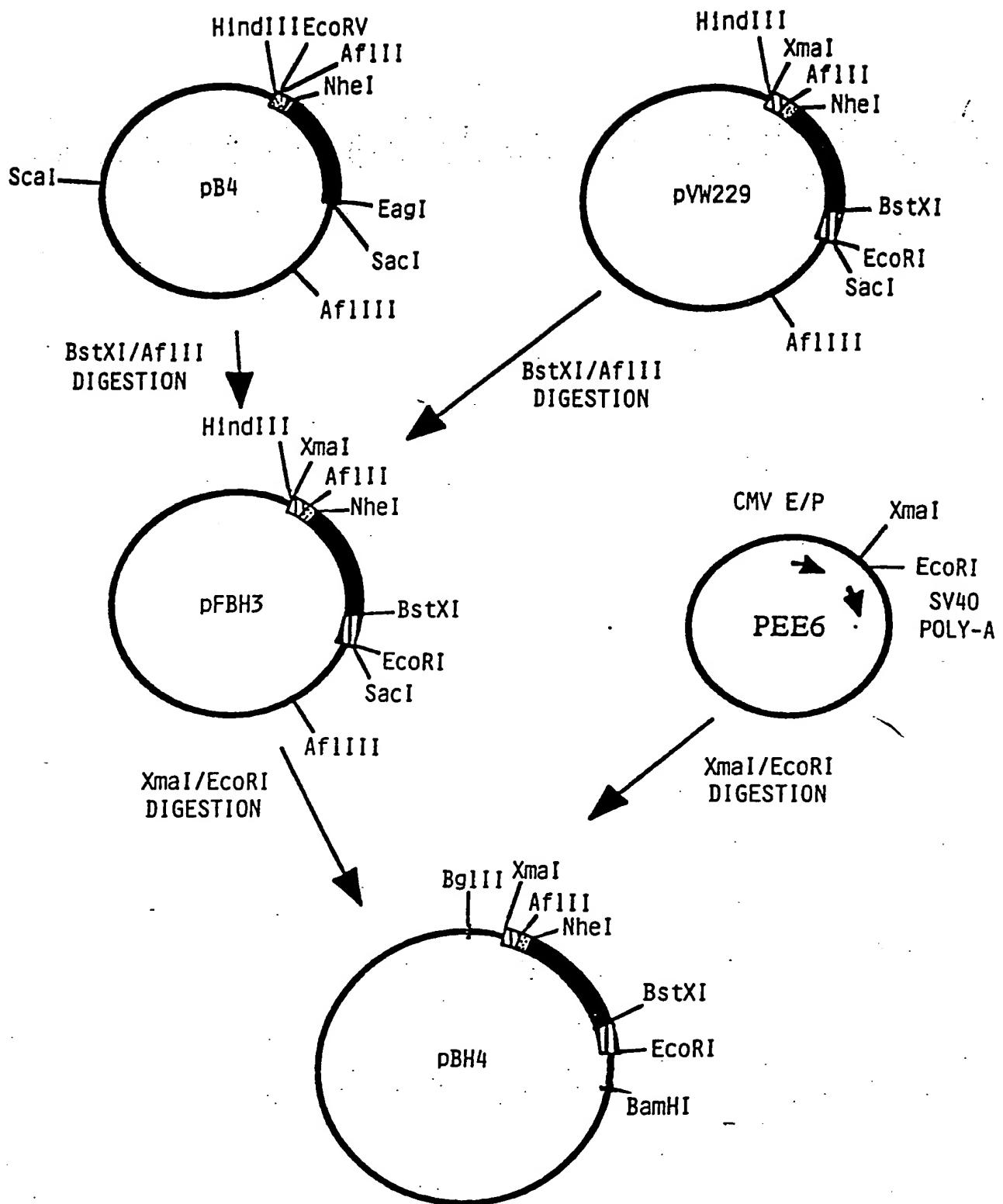


FIG. 19F

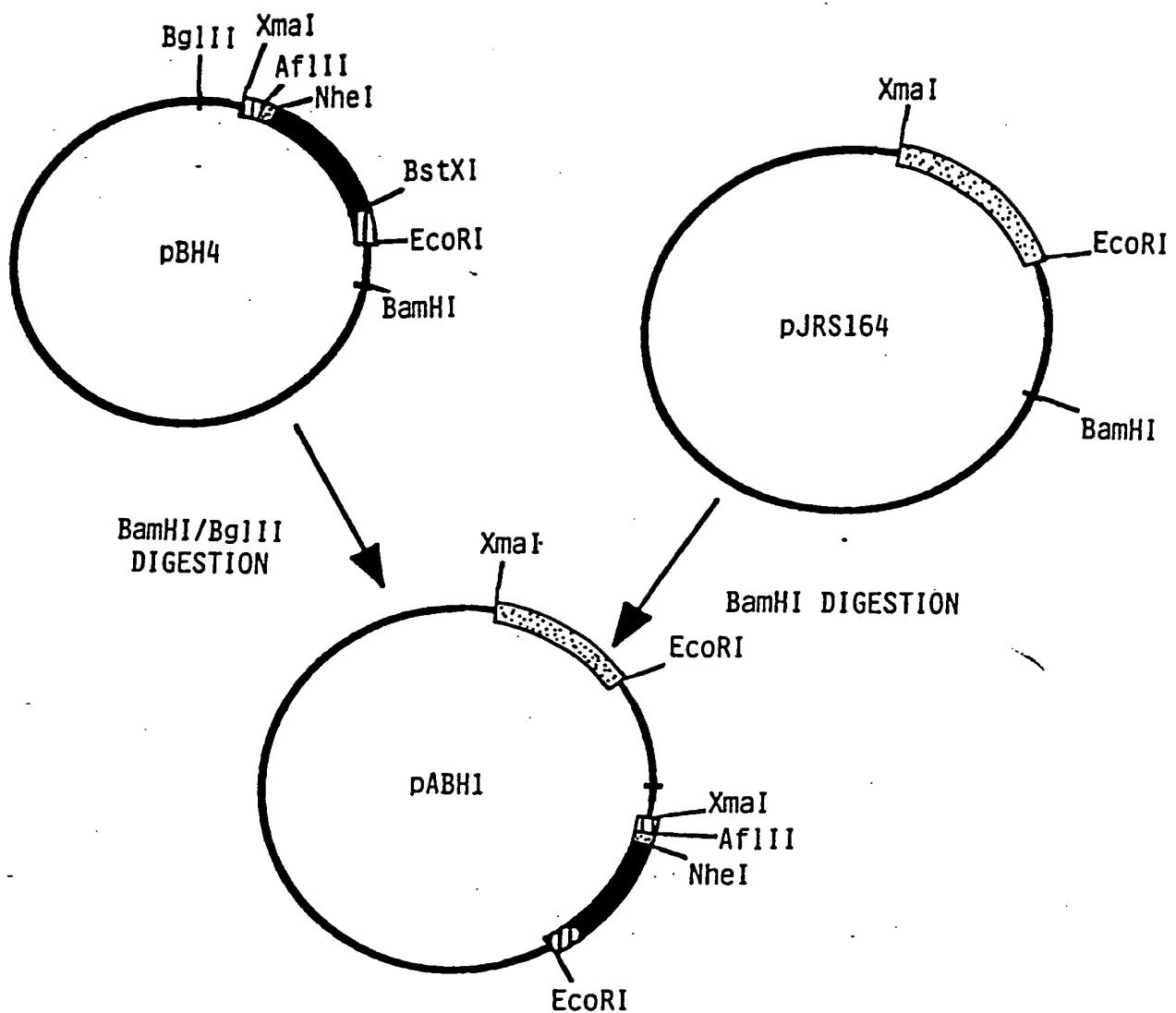


FIG. 19G

OPR132

I-A^d β signal peptide front primer with Kozak consensus for CellTech vector -

HindIII/XmaI sites

5'-CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA
GC-3'

OPR133

I-A^d β signal peptide back primer with Kozak consensus for CellTech vector - AfIII site

5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134

I-A^d β transmembrane front primer for CellTech vector - BstXI sites

5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135

I-A^d β transmembrane back primer for CellTech vector - SstI, EcoRI sites

5'-CCC CCC GAG CTC GAA TCC TCA CTG CAG GAG CCC TGC TGG-3'

OPR136

I-A^d α signal peptide front primer with Kozak consensus for CellTech vector -

HindIII/XmaI sites

5'-CCC CCC AAG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC
TG-3'

OPR139

I-A^d α transmembrane primer for CellTech vector - SstI/EcoRI sites

5'-CCC CCC GAG CTC GAA TCC TCA TAA AGG CCC TGG GTG TCT G-3'

B7-1-2F

Murine B7-1 front primer with Kozak consensus for CloneTech vector - NotI site

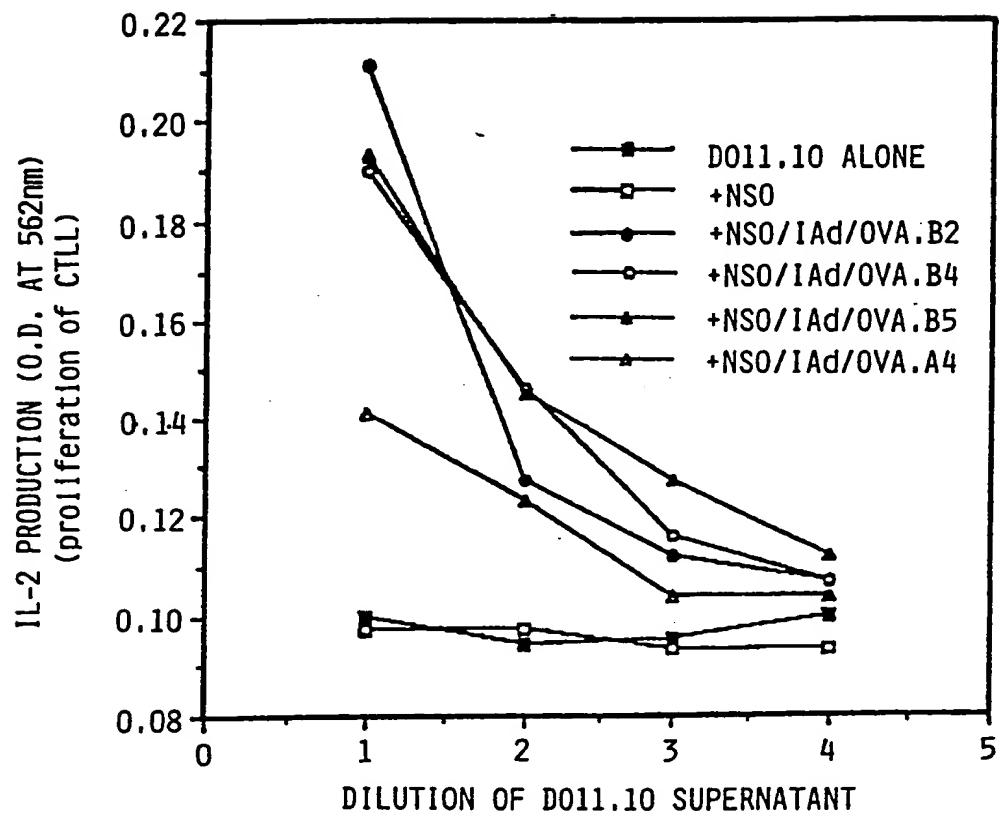
5'-CCC CCC CCG CGG CCG CCC CAC CAT GGG ACT GAG TAA CAT TCT
C-3'

B7-1-2B

Murine B7-1 BACK primer for CloneTech vector - NotI site

5'-CCC CCC GCG GCC GCT TTA AAA ACA TGT ATC ACT TTT-3'

FIG. 20



RECEIVED "THIRTYTHREEGO"

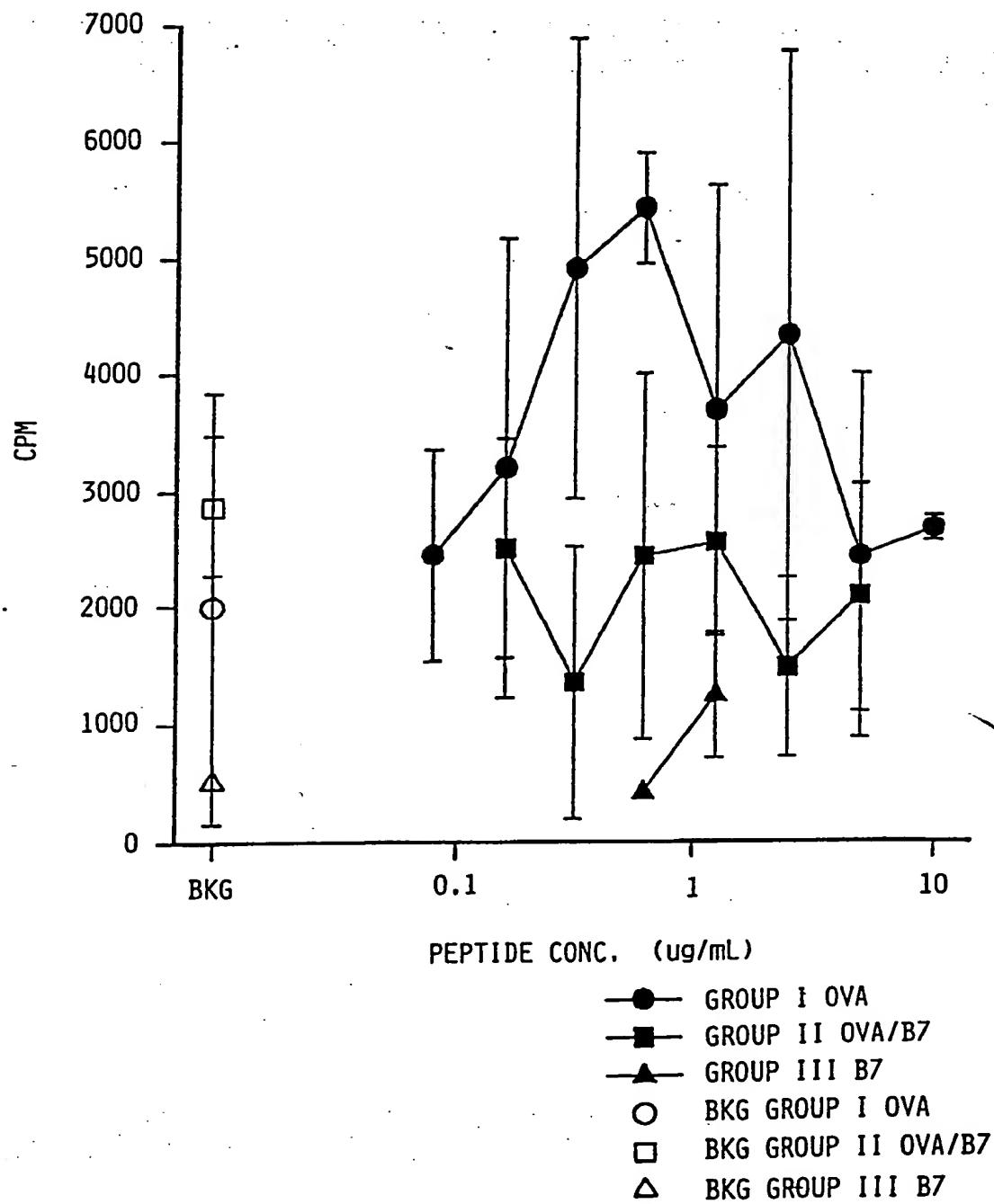


FIG. 22

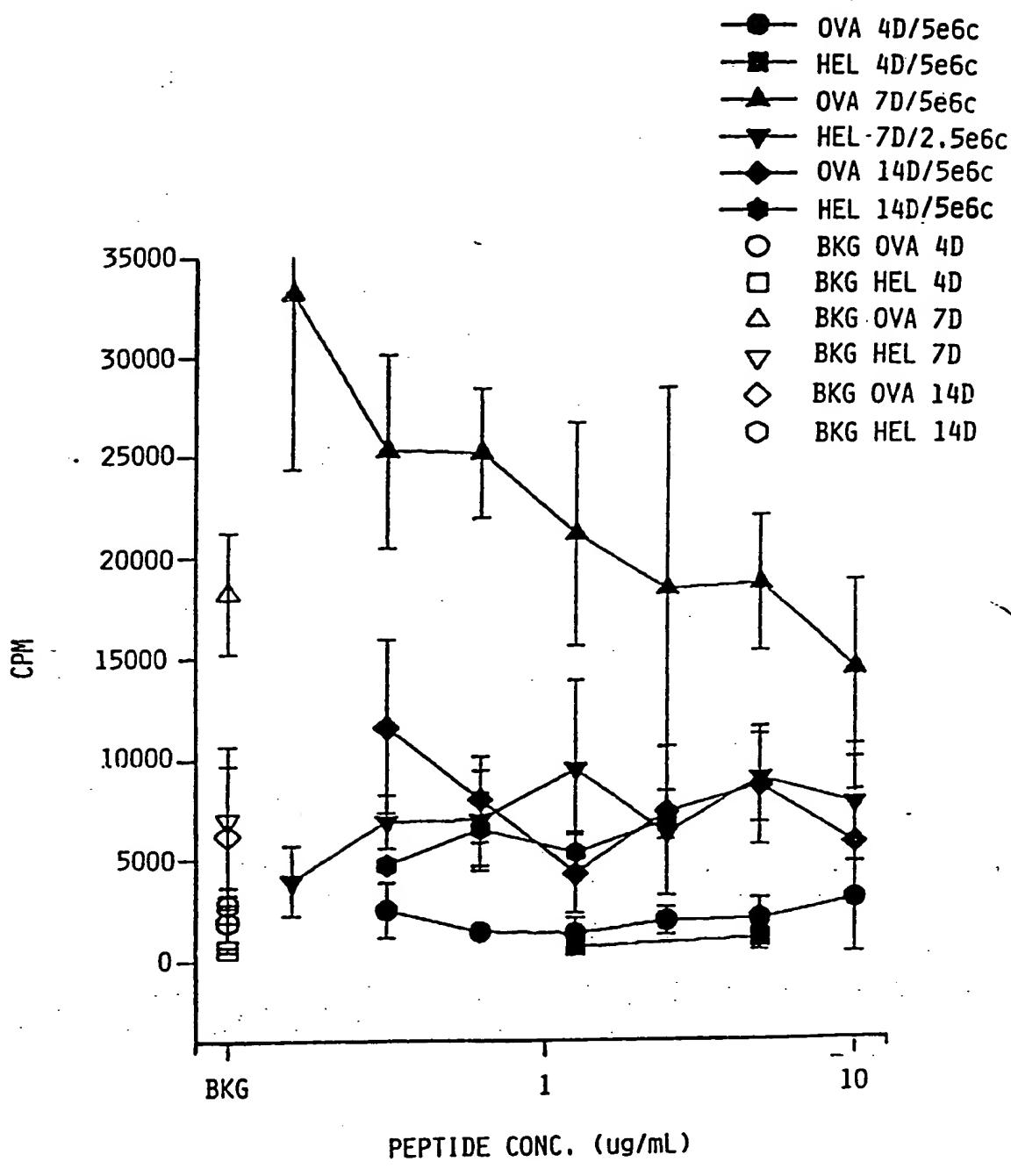


FIG. 23

09848164 050304

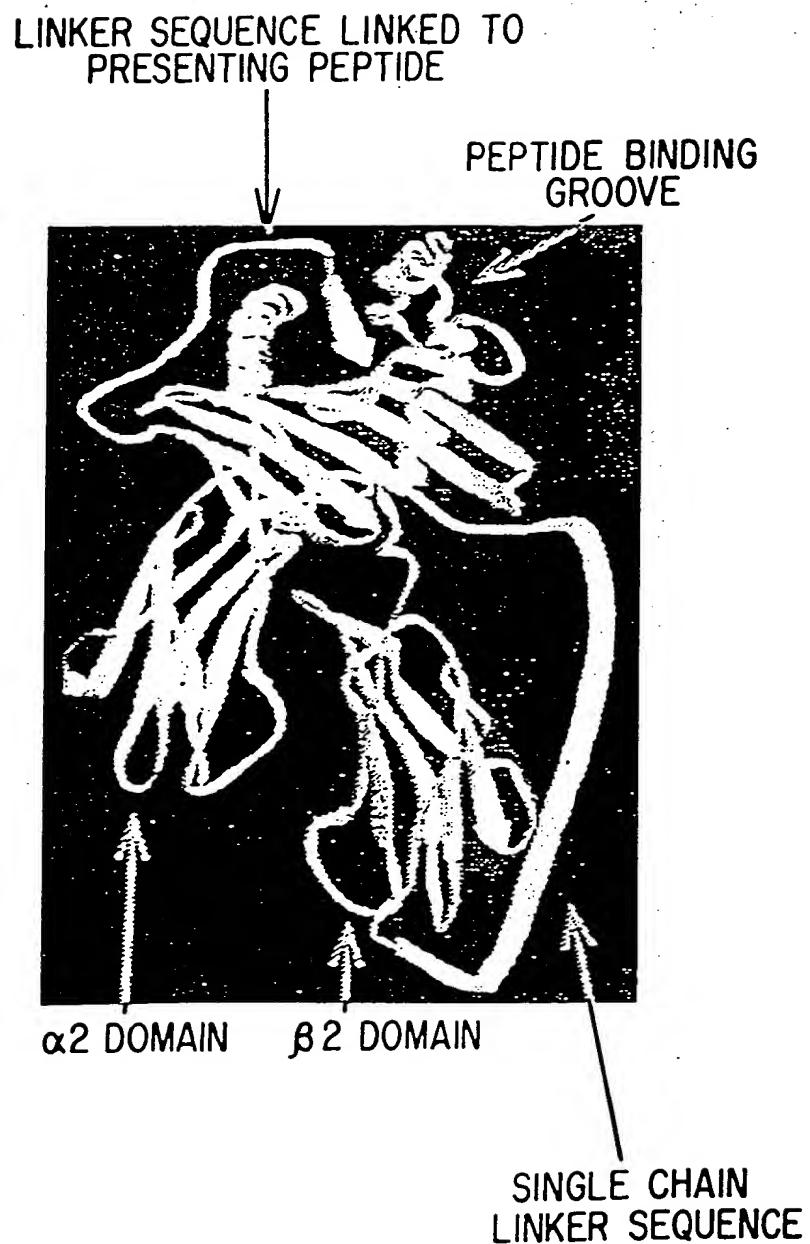


FIG. 24

DRAFT - 4/20/96

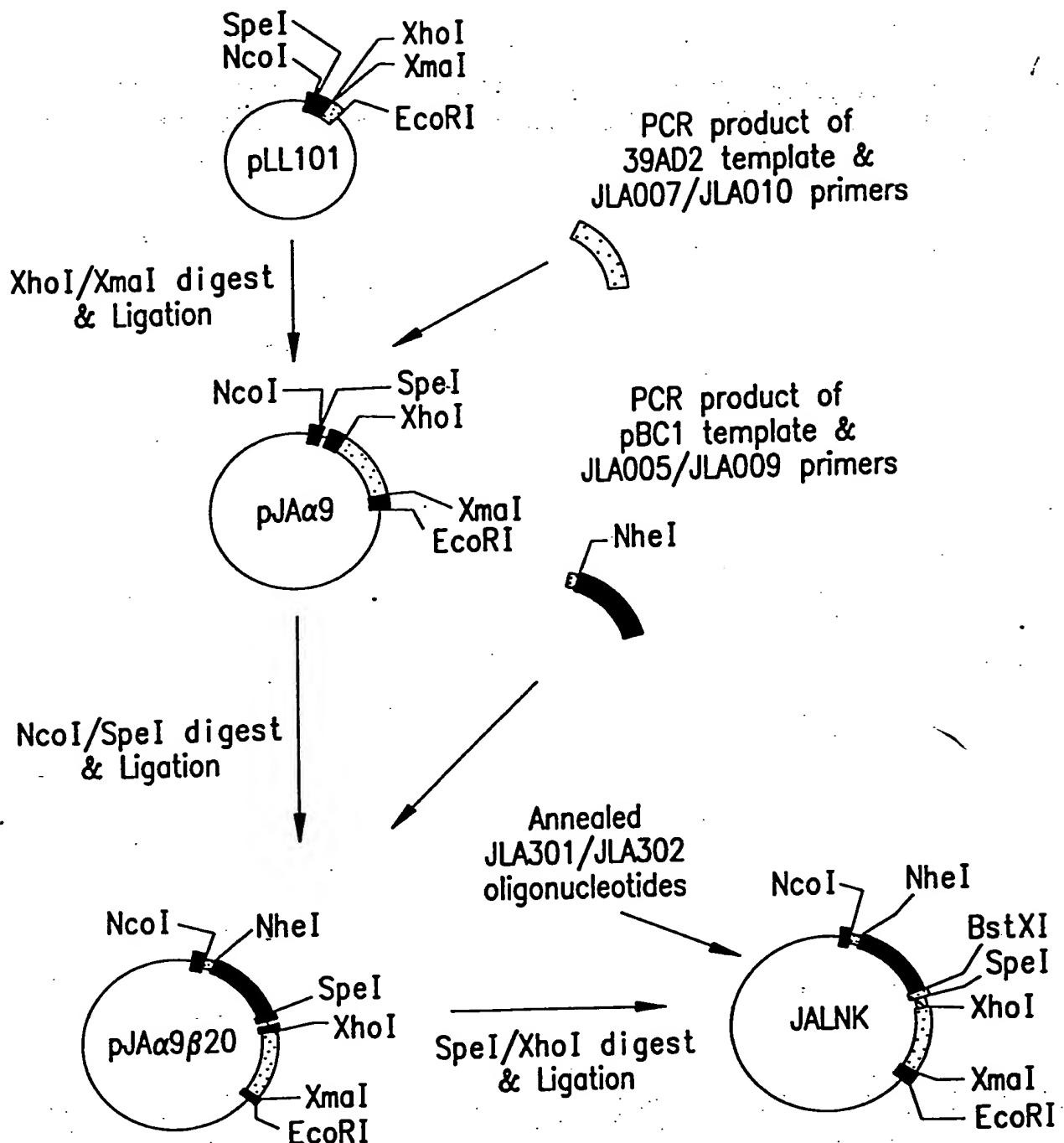


FIG.25A

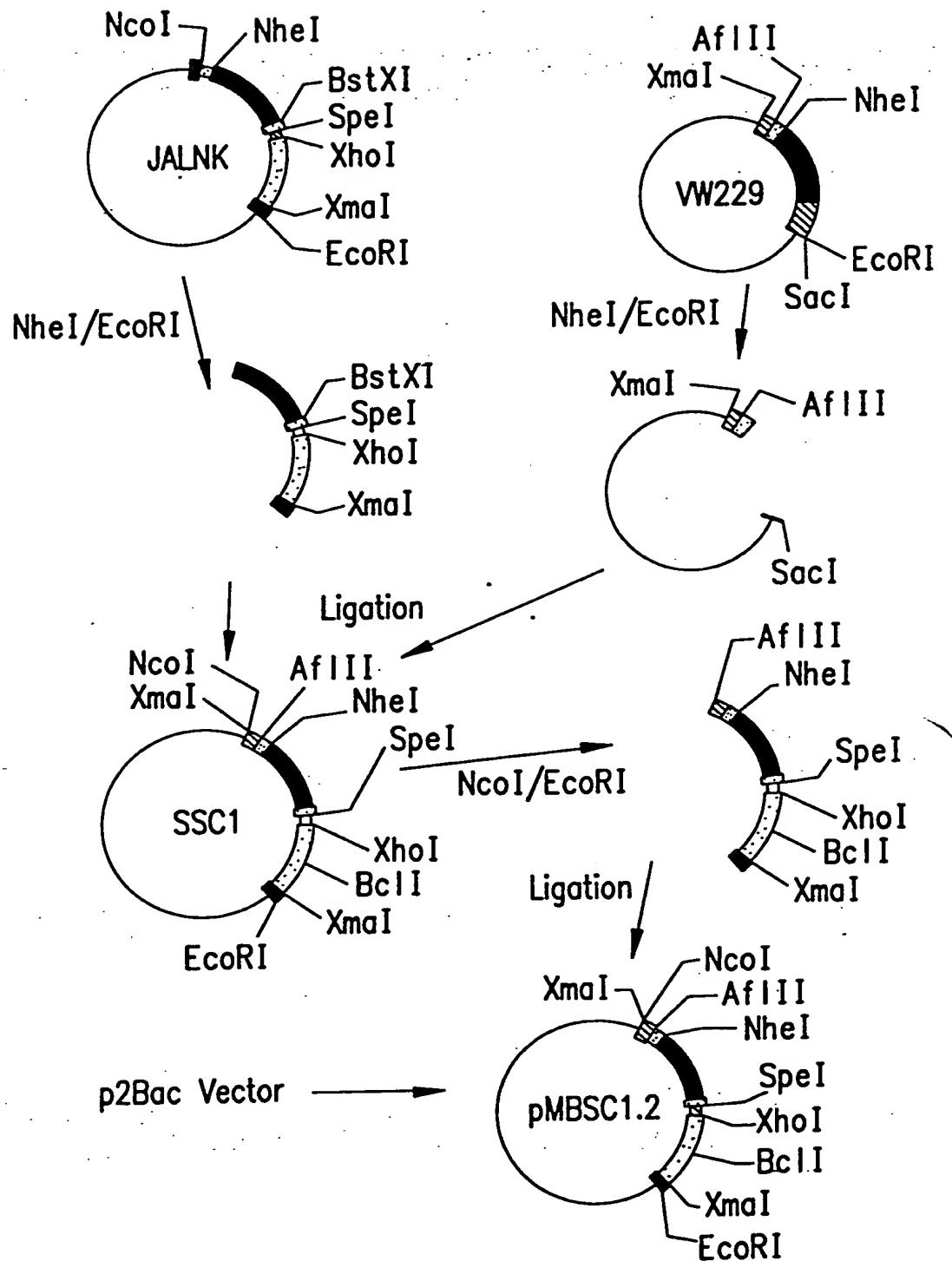


FIG.25B

DRAFT - DO NOT CITE

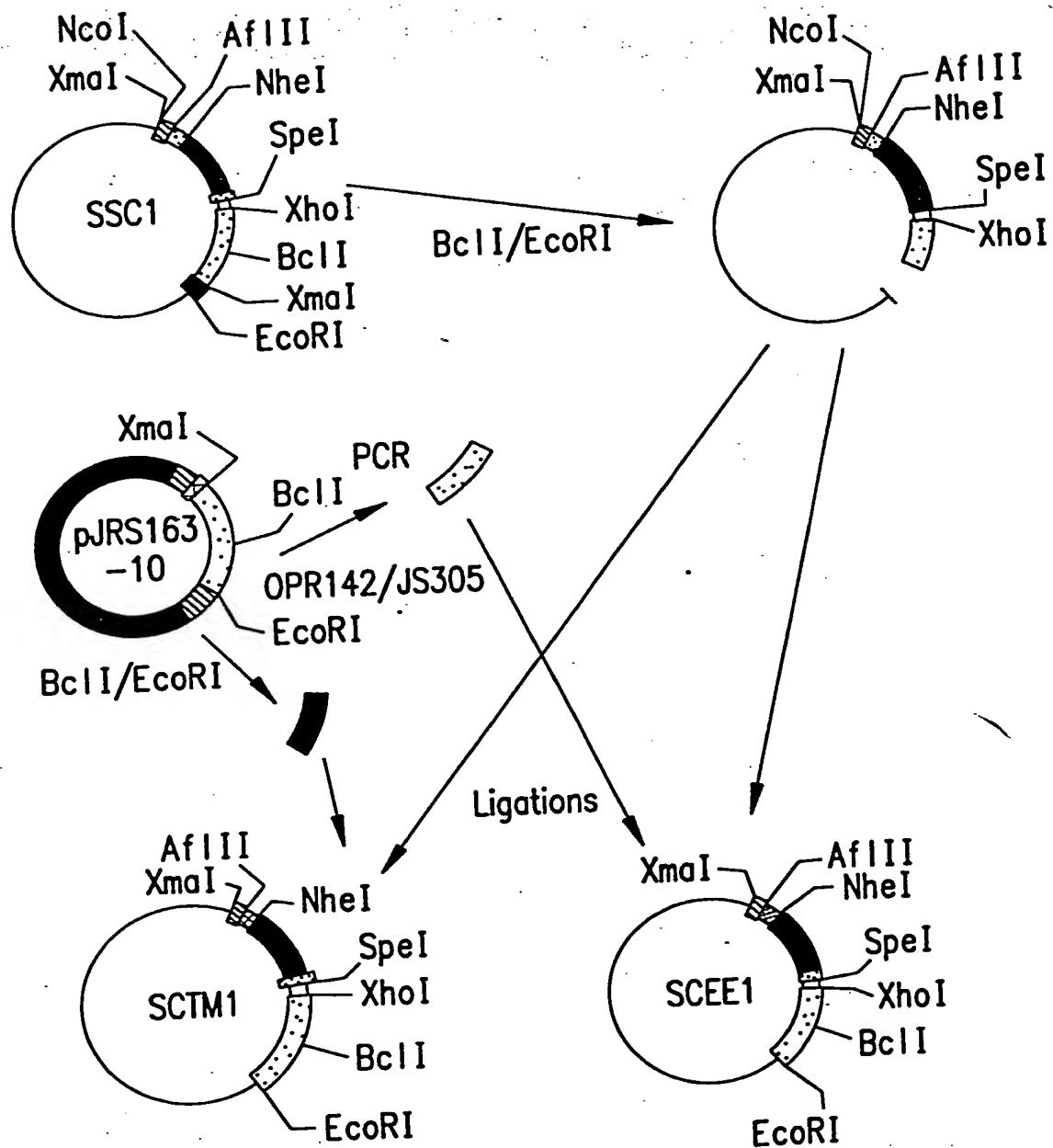


FIG.25C

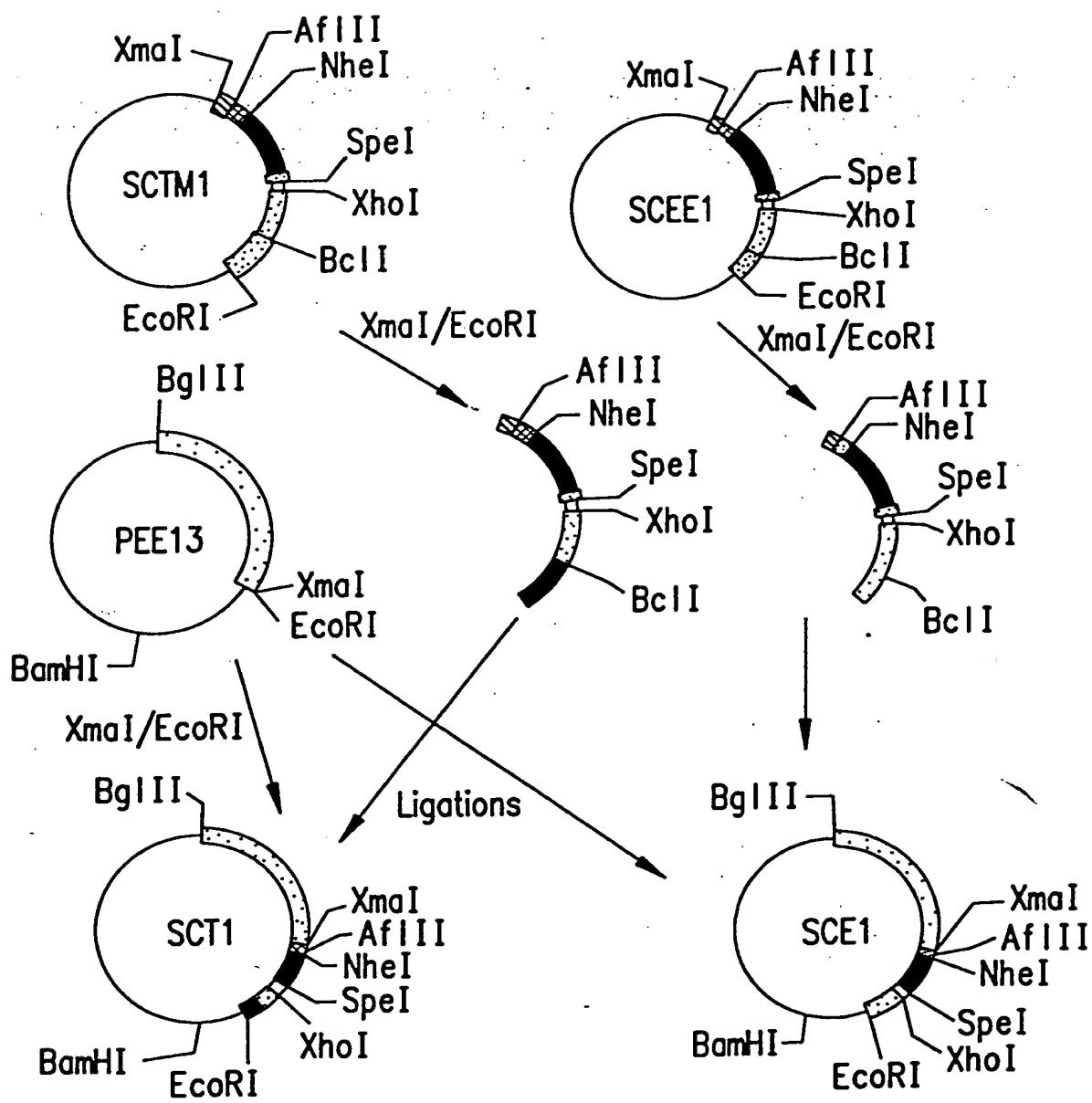


FIG.25D

JLA-005

5'-CCCCCCGCCATGGCCGCTAGCGGAGGGGGCGGAAGC-3'

JLA-007

5'-CCCGGGGCCTCGAGTGAAGACGACATTGAGGCCGAC-3'

JLA-009

5'-CCCCCCCACACTAGTCCACTCCACAGTGATGGGCT-3'

JLA-010

5'-CCCCCCCCCGGGACCAAGTGTTCAGAACCGGCTCCTC-3'

JLA-301

5'-TCGAGGAACCGCCACCGCCAGAACCGCCGCCACCGGA-
ACCACCAACGCCGCTGCCACCGCCACCA-3'

JLA-302

5'-CTAGTGGTGGCGGTGGCAGCGGCGGTGGTGGTTCCGG-
TGGCGGCGGTTCTGGCGGTGGCGGTTCC-3'

OPR-142

5'-CTTGGGAATCTTACTAAGAGG-3'

JS-305

5'-CAGGTCGAATTCTCATTCCATCGGCATGTACTCTTCTT-
CCTCCCAGTGTTCAGAACCGG-3'

FIG.26

47/69

10 20 30 40 50
* * * * *

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
M A L Q I P S L L L S A A V V>
----- I-Ad β CHAIN LEADER -----

60 70 80 90
* * * *

GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
V L M V L S S P R T L S I S Q A>

100 110 120 130 140
* * * * *

GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
V H A A H A E I N E A G R A S G>
----- OVA 323-339 -----><

150 160 170 180 190
* * * * *

GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
G G G S G G G N S E R H F V V>

-- 10 AMINO ACID LINKER-->----- I-Ad β -1 DOMAIN -----

200 210 220 230 240
* * * * *

CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
Q F K G E C Y Y T N G T Q R I R>

250 260 270 280 290
* * * * *

CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
L V T R Y I Y N R E E Y V R Y D>

FIG.27A

300 * 310 * 320 * 330 *
 AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
 TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
 S D V G E Y R A V T E L G R P D>

340 * 350 * 360 * 370 * 380 *
 GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
 CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
 A E Y W N S Q P E I L E R T R A>

390 * 400 * 410 * 420 * 430 *
 GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
 CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
 E V D T A C R H N Y E G P E T S>

440 * 450 * 460 * 470 * 480 *
 ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
 TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
 T S L R R L E Q P N V A I S L S>
 --- I-Ad β -1 DOMAIN -><--- I-Ad β -2 DOMAIN ---

490 * 500 * 510 * 520 * 530 *
 AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
 TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
 R T E A L N H H N T L V C S V T>

540 * 550 * 560 * 570 *
 GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
 CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
 D F Y P A K I K V R W F R N G Q>

580 590 600 610 620
 * * * * *
 GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
 CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
 E E T V G V S S T Q L I R N G D>

630 640 650 660 670
 * * * * *
 TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
 ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
 W T F Q V L V M L E M T P H Q G>

680 690 700 710 720
 * * * * *
 GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
 CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
 E V Y T C H V E H P S L K S P I>
 ----- I-Ad β -2 DOMAIN -----

730 740 750 760 770
 * * * * *
 ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
 TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
 T V E W T S G G G G S G G G G G S>
 -----><----- 24 AMINO ACID LINKER -----

780 790 800 810
 * * * *
 GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT
 CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
 G G G G S G G G G S S S E D D I>
 -----><-----

820 830 840 850 860
 * * * * *
 GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
 CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E A D H V G F Y G T T V Y Q S P>
 ----- I-Ad α -1 DOMAIN -----

50/69

870 880 890 900 910
* * * * *

GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
G D I G Q Y T H E F D G D E L F>

920 930 940 950 960
* * * * *

TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
Y V D L D K K K T V W R L P E F>

970 980 990 1000 1010
* * * * *

GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
G Q L I L F E P Q G G L Q N I A>

1020 1030 1040 1050
* * * *

GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
A E K H N L G I L T K R S N F T>

I-Ad α -1 DOMAIN

1060 1070 1080 1090 1100
* * * * *

CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
P A T N E A P Q A T V F P K S P>

I-Ad α -2 DOMAIN

1110 1120 1130 1140 1150
* * * * *

GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
V L L G Q P N T L I C F V D N I>

FIG.27D

51/69

TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
F P P V I N I T W L R N S K S V>

1210 1220 1230 1240 1250
* * * * *

ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
T D G V Y E T S F L V N R D H S>

1260 1270 1280 1290
* * * *

TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
F H K L S Y L T F I P S D D D D I>

1300 1310 1320 1330 1340
* * * *

TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
Y D C K V E H W G L E E P V L K>

1350 1360 1370 1380

FIG. 27E

10 20 30 40 50
 * * * * *
 CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC TCA GCT GCT GTG GTG
 GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG AGT CGA CGA CAC CAC
 M A L G I P S L L L S A A V V>
 <----- I-Ad β CHAIN LEADER ----->

60 70 80 90
 * * * * *
 GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
 CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
 V L M V L S S P R T L S I S Q A>
 -----><-----

100 110 120 130 140
 * * * * *
 GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
 CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
 V H A A H A E I N E A G R A S G>
 ----- OVA 323-339 -----><-----

150 160 170 180 190
 * * * * *
 GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
 CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
 G G G S G G G N S E R H F V V>
 -- 10 AMINO ACID LINKER --><----- I-Ad β -1 DOMAIN ----->

200 210 220 230 240
 * * * * *
 CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
 GTC AAG TTC CCG CTC ACG ATG ATG TCC TTG CCC TGC GCG TAT GCC
 Q F K G E C Y Y T N G T Q R I R>

250 260 270 280 290
 * * * * *
 CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
 GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
 L V T R Y I Y N R E E Y V R Y D>

300 310 320 330
 * * * *
 AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
 TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
 S D V G E Y R A V T E L G R P D>

340 350 360 370 380
 * * * * *
 GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
 CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
 A E Y W N S Q P E I L E R T R A>

390 400 410 420 430
 * * * * *
 GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
 CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
 E V D T A C R H N Y E G P E T S>

440 450 460 470 480
 * * * * *
 ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
 TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
 T S L R R L E Q P N V A I S L S>
 --- I-Ad β -1 DOMAIN -><--- I-Ad β -2 DOMAIN ---

490 500 510 520 530
 * * * * *
 AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
 TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
 R T E A L N H H N T L V C S V T>

540 550 560 570
 * * * *
 GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
 CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
 D F Y P A K I K V R W F R N G Q>

580 590 600 610 620
 * * * * *
 GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
 CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
 E E T V G V S S T Q L I R N G D>

630 640 650 660 670
 * * * * *
 TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
 ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
 W T F Q V L V M L E M T P H Q G>

680 690 700 710 720
 * * * * *
 GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
 CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
 E V Y T C H V E H P S L K S P I>
 ----- I-Ad β -2 DOMAIN -----

730 740 750 760 770
 * * * * *
 ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
 TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
 T V E W T S G G G G S G G G G S>
 ----- ><----- 24 AMINO ACID LINKER -----

780 790 800 810
 * * * *
 GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAG GAC ATT
 CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
 G G G G S G G G S S S E D D I>
 ----- ><-----

820 830 840 850 860
 * * * * *
 GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
 CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E A D H V G F Y G T T V Y Q S P>
 ----- I-Ad α -1 DOMAIN -----

870 880 890 900 910
 * * * * *
 GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
 CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
 G D I G Q Y T H E F D G D E L F>

920 930 940 950 960
 * * * * *
 TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
 ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
 Y V D L D K K K T V W R L P E F>

970 980 990 1000 1010
 * * * * *
 GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
 CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
 G Q L I L F E P Q G G L Q N I A>

1020 1030 1040 1050
 * * * *
 GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
 CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
 A E K H N L G I L T K R S N F T>
 I-Ad α -1 DOMAIN

1060 1070 1080 1090 1100
 * * * * *
 CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
 GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
 P A T N E A P Q A T V F P K S P>
 I-Ad α -2 DOMAIN

1110 1120 1130 1140 1150
 * * * * *
 GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
 CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
 V L L G Q P N T L I C F V D N I>

1160 1170 1180 1190 1200
 * * * * *

TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
 AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
 F P P V I N I T W L R N S K S V>

1210 1220 1230 1240 1250
 * * * * *

ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
 TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
 T D G V Y E T S F L V N R D H S>

1260 1270 1280 1290
 * * * *

TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
 AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
 F H K L S Y L T F I P S D D D I>

1300 1310 1320 1330 1340
 * * * * *

TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
 ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
 Y D C K V E H W G L E E P V L K>

----- I-Ad α -2 DOMAIN -----

1350 1360 1370 1380 1390
 * * * * *

CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT
 GTG ACC CTT GGA CTC TAA GGT CGG GGG TAC AGT CTC GAC TGT CTT TGA
 H W E P E I P A P M S E L T E T>

-----><----- I-Ad α -TM DOMAIN -----

1400 1410 1420 1430 1440
 * * * * *

GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG
 CAC CAC ACA CGG GAC CCC AAC AGA CAC CCG GAA CAC CCG TAG CAC CAC
 V V C A L G L S V G L V G I V V>

1450

*

1460

*

1470

*

1480

*

1490

*

GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA
 CCG TGG TAG AAG TAG TAA GTT CCG GAC GCT AGT CCA CCG TGG AGG TCT
 G T I F I I Q G L R S G G T S R>

 CAC CCA GGG CCT TTA TGA
 GTG GGT CCC GGA AAT ACT
 H P G P L *->
 - I-Ad α -TM DOMAIN ->

103050-4-131860

FIG.28F

10 20 30 40 50
* * * * *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG AGT CGA CGA CAC CAC
M A L Q I P S L L L S A A V V>
<----- I-Ad β CHAIN LEADER ----->

60 70 80 90
* * * *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
V L M V L S S P R T L S I S Q A>
-----><-----

100 110 120 130 140
* * * * *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
V H A A H A E I N E A G R A S G>
----- OVA 323-339 -----><-----

150 160 170 180 190
* * * * *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
G G G S G G G N S E R H F V V>
-- 10 AMINO ACID LINKER --><----- I-Ad β -1 DOMAIN ----->

200 210 220 230 240
* * * * *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
Q F K G E C Y Y T N G T Q R I R>

250 260 270 280 290
* * * * *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
L V T R Y I Y N R E E Y V R Y D>

300

310

320

330

*

*

*

*

AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
 TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
 S D V G E Y R A V T E L G R P D>

340

350

360

370

380

*

*

*

*

*

GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
 CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
 A E Y W N S Q P E I L E R T R A>

390

400

410

420

430

*

*

*

*

*

GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
 CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
 E V D T A C R H N Y E G P E T S>

440

450

460

470

480

*

*

*

*

*

ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
 TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
 T S L R R L E Q P N V A I S L S>
 --- I-Ad β -1 DOMAIN -><---- I-Ad β -2 DOMAIN -----

490

500

510

520

530

*

*

*

*

*

AGG ACA GAG GCC CTC AAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
 TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
 R T E A L N H H N T L V C S V T>

540

550

560

570

*

*

*

*

GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
 CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
 D F Y P A K I K V R W F R N G Q>

60/69

580 590 600 610 620
* * * * *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
E E T V G V S S T Q L I R N G D>

630 640 650 660 670
* * * * *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
W T F Q V L V M L E M T P H Q G>

680 690 700 710 720
* * * * *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
E V Y T C H V E H P S L K S P I>
----- I-Ad β -2 DOMAIN -----

730 740 750 760 770
* * * * *
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
T V E W T S G G G G S G G G G S>
-----><----- 24 AMINO ACID LINKER -----

780 790 800 810
* * * *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
G G G G S G G G S S S E D D I>
-----><-----

820 830 840 850 860
* * * * *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
E A D H V G F Y G T T V Y Q S P>
----- I-Ad α -1 DOMAIN -----

FIG.29C

61/69

870 880 890 900 910
* * * * *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
G D I G Q Y T H E F D G D E L F>

920 930 940 950 960
* * * * *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
Y V D L D K K K T V W R L P E F>

970 980 990 1000 1010
* * * * *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA GCT GAC GTT TTG TAT CGA
G Q L I L F E P Q G G L Q N I A>

1020 1030 1040 1050
* * * *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
A E K H N L G I L T K R S N F F>
----- I-Ad α -1 DOMAIN -----

1060 1070 1080 1090 1100
* * * * *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
P A T N E A P Q A T V F P K S P>
-----><----- I-Ad α -2 DOMAIN -----

1110 1120 1130 1140 1150
* * * * *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
V L L G Q P N T L I C F V D N I>

FIG.29D

62/69

1160

*

1170

*

1180

*

1190

*

1200

*

TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
F P P V I N I T W L R N S K S V>

1210

*

1220

*

1230

*

1240

*

1250

*

ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
T D G V Y E T S F L V N R D H -S>

1260

*

1270

*

1280

*

1290

*

TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
F H K L S Y L T F I P S D D D I>

1300

*

1310

*

1320

*

1330

*

1340

*

TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
Y D C K V E H W G L E E P V L K>

I-Ad α -2 DOMAIN

1350

*

1360

*

1370

*

1380

*

CAC TGG GAG GAA GAA GAG TAC ATG CCG ATG GAA TGA
GTG ACC CTC CTT CTC ATG TAC GGC TAC CTT ACT

H

W

E

E

E

E

Y

M

P

M

E

*>

EE TAG

FIG.29E

印譜集卷之三

Sequence alignment diagram showing the alignment of the OVA 323-339 peptide with the IAd β chain signal peptide. The OVA peptide sequence is aligned with the signal peptide sequence, with the peptide linker and β 1- β 2 domains indicated. The alignment shows high conservation between the two sequences, with the peptide linker and β 1- β 2 domains being the most divergent regions.

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FIG. 30

64/69

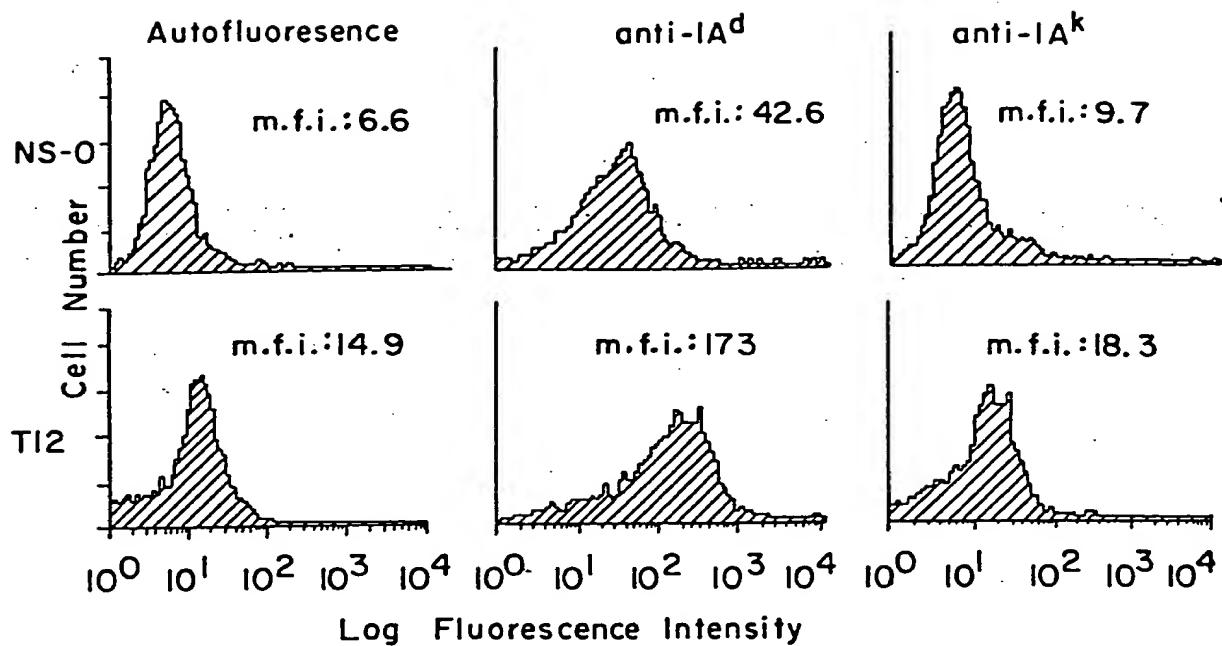


FIG. 3IA

FIG. 3IA 64/69

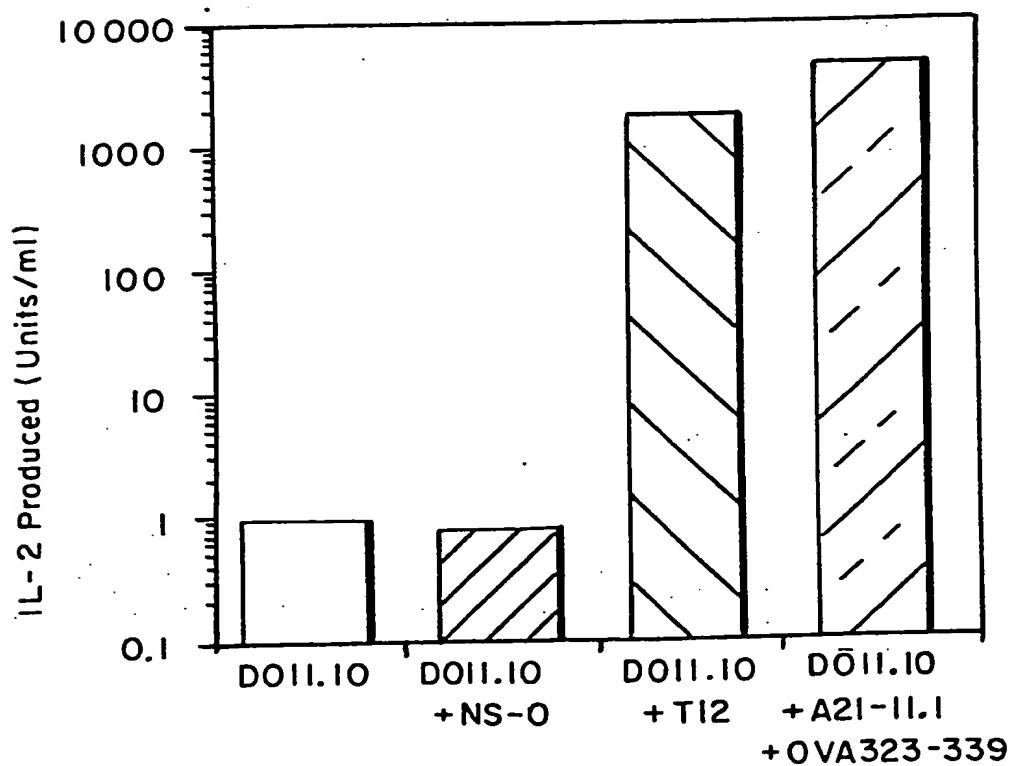


FIG. 3IB

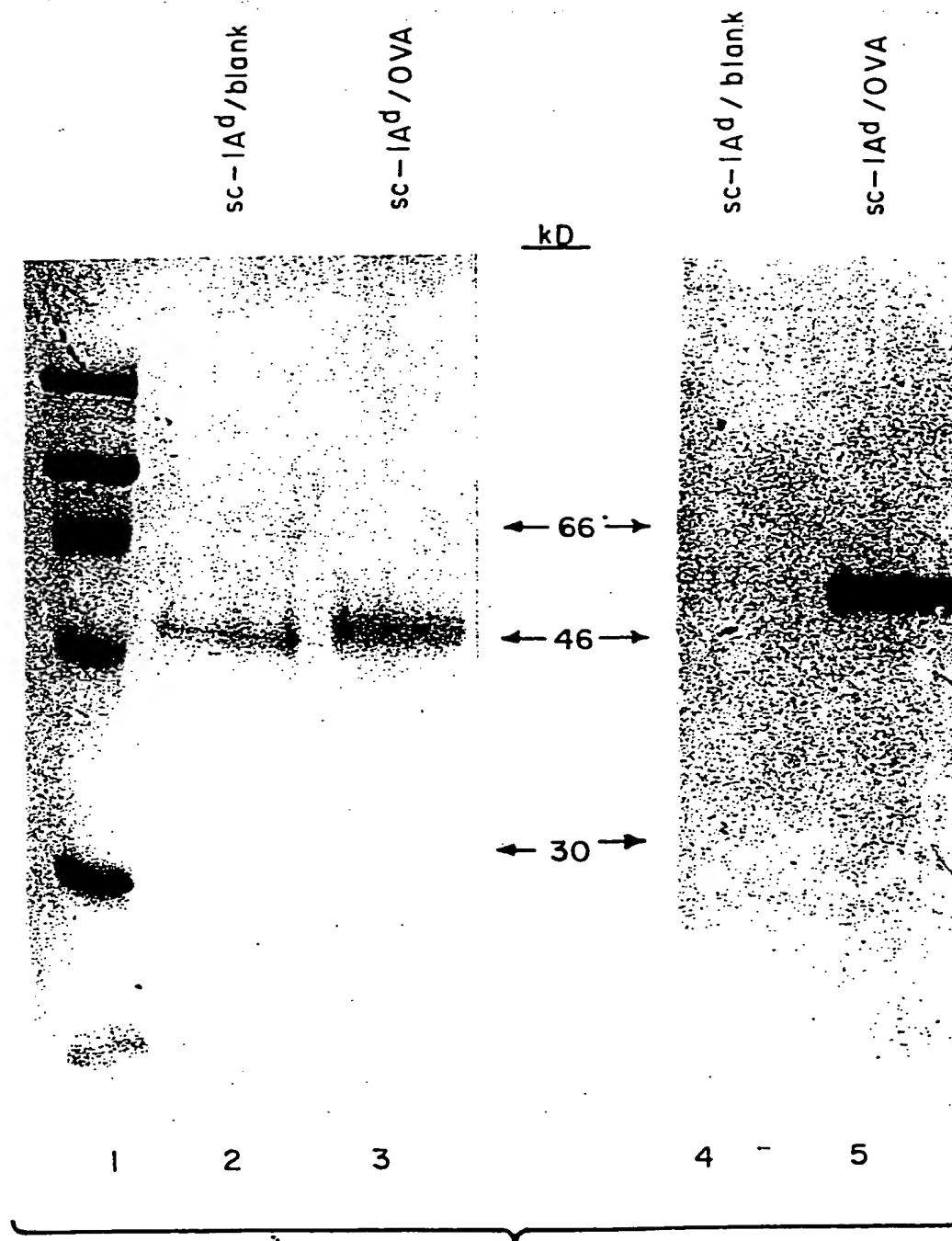


FIG.32

FIG. 33

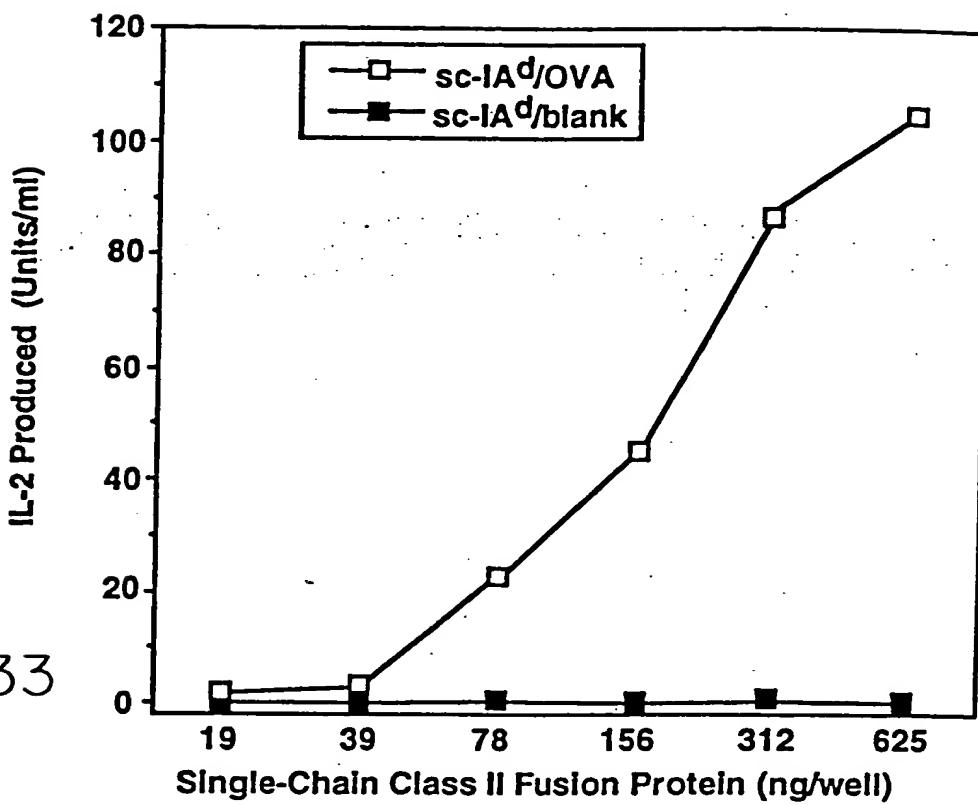


FIG. 34C

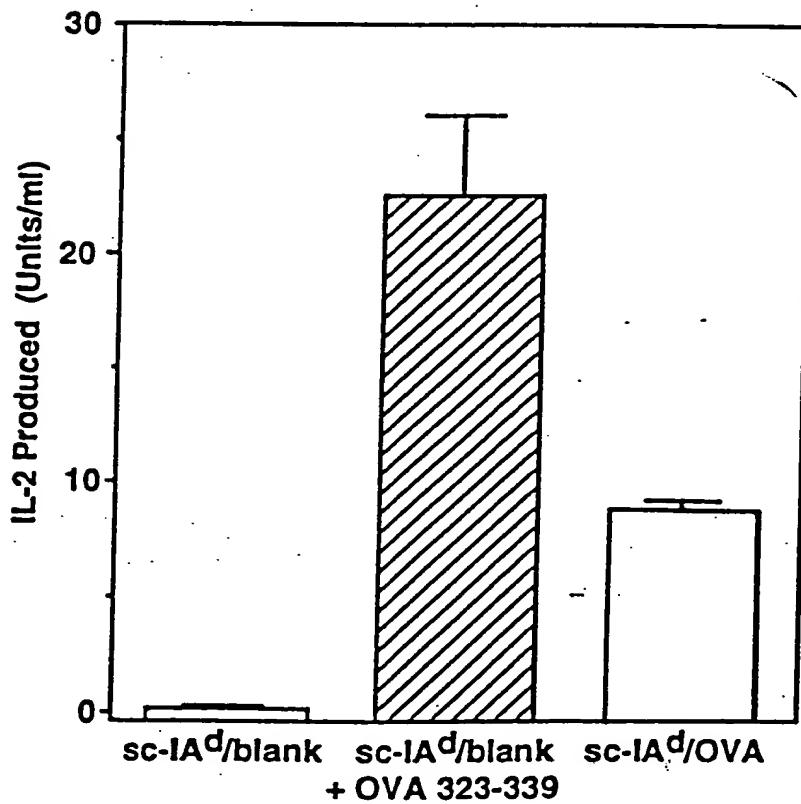


FIG.34A

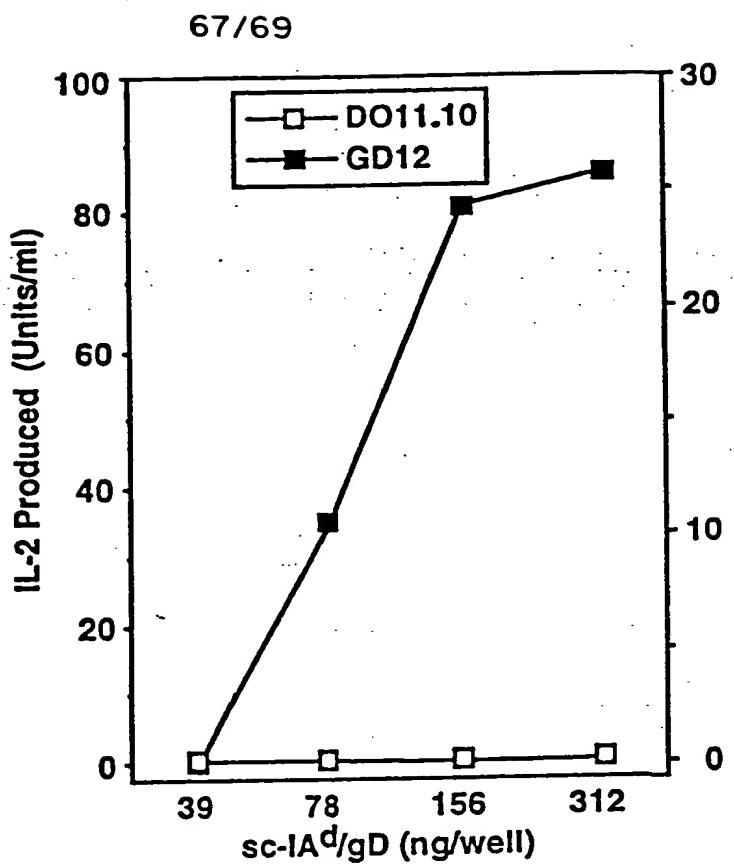
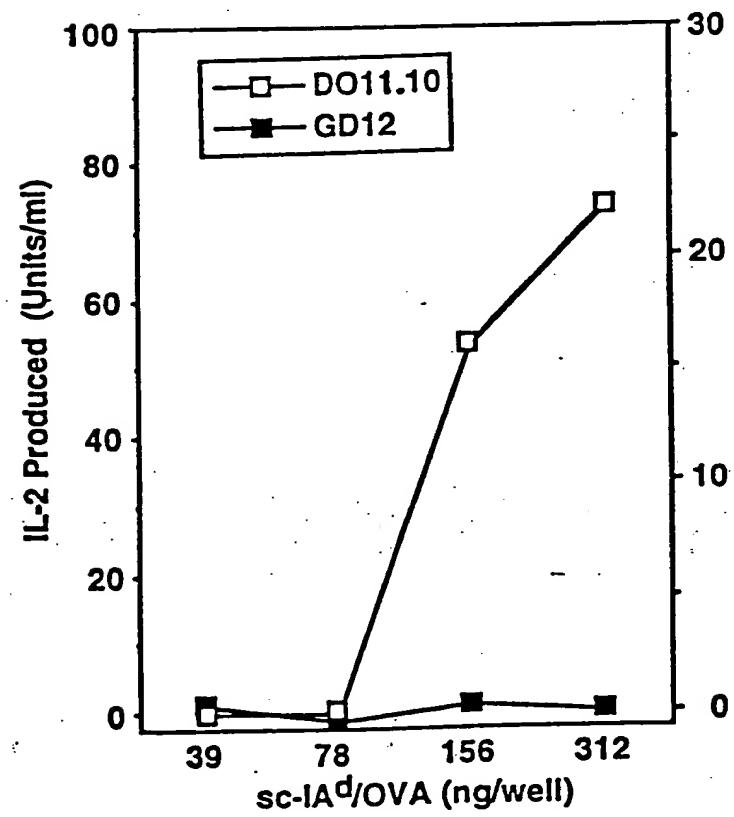


FIG.34B



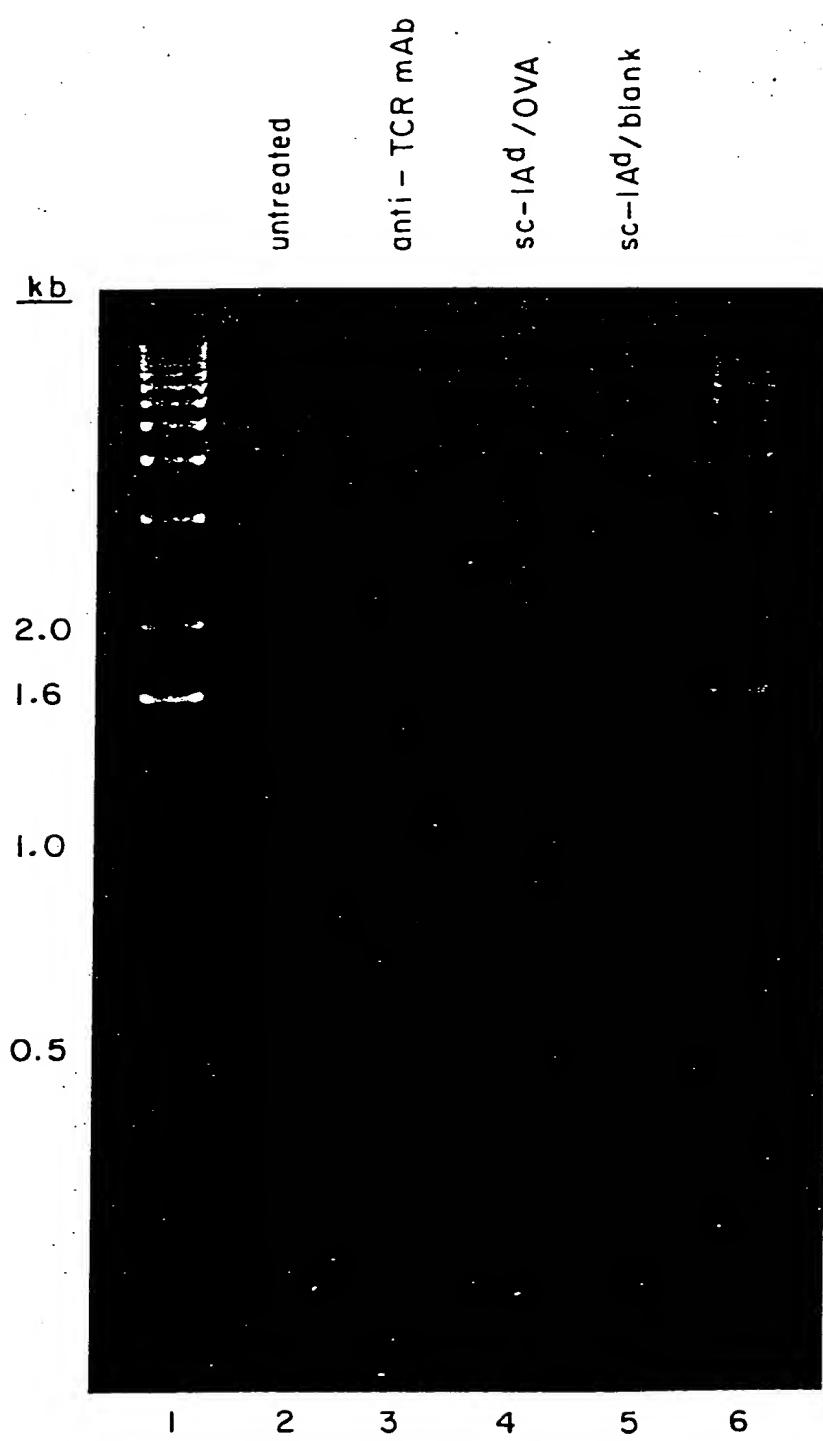
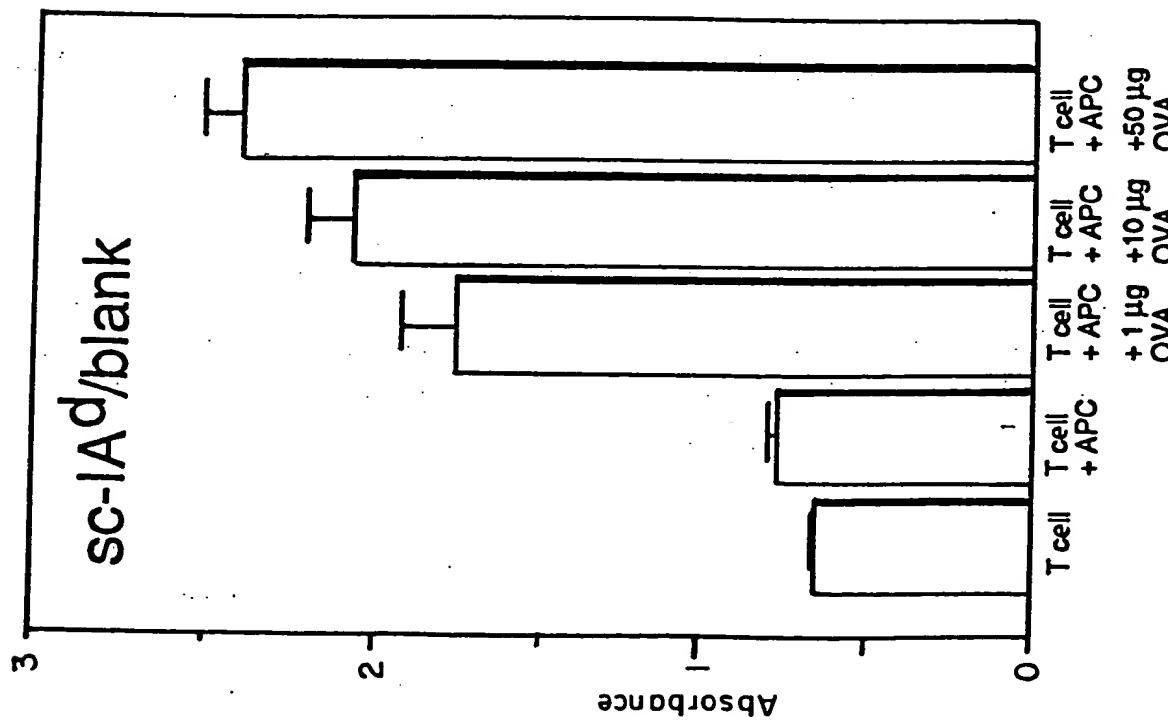


FIG. 35



SC-IAd/OVA

